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Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.
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N-PSDB; AAD37441.
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5.1.6
Compugen Ltd
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GenCore version
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Listing first 45 summaries
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ADK83174
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AAU00471
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ABR48229
ABU56613
ABP97212
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ADM42033
ADN38748
ADK83210
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Human, nectin-Jalpha, therapy, cell adhesion, cell proliferation, sepsis, paracellular transport disorder; kidney; diabetic retinopathy, allergy, allograft rejection; metastasis, restenosis; inflammatory bowel disease; oedema, atherosclerosis; ischaemia reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Youakim A;
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                                                                                                                                                                                                                     Mouse nectin-3-human nectin 3alpha fusion protein.
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/note= "Mouse nectin-3 protein"
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AAE23282 standard; protein; 549 AA
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AAE23283 standard; protein; 549 AA.

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gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial adhesion activity, adherens junction formation activity, epithelial or cc andothelial barrier function activity, endothelial proliferation or cm migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above condethelial barrier function disorder which is treated by the above asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as stroke, restenosis, tumour growth and treating herpesvirus infection.

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

CC smoothelial cell, an epithelial cell or a smooth muscle cell (vascular conduction) and numan nectin-3alpha protein. Human nectin-3 and human nectin-3alpha protein. Human nectin-3 alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
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Claim 1; Page 80-82; 141pp; English
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RESULT 2 AAE23283

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The invention relates to a substantially purified nectinalsha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endiding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, paracellular transport disorders such as massarais of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for
                                                                                                                                                             Human, nectin-Jalpha, therapy, cell adhesion, cell proliferation, sepsis, paracellular transport disorder; kidney, diabetic retinopathy, allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema, atherosclerosis; ischemia.reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
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inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, etroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithalial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3alpha gene is located on chromosome 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLLFPLLLLFSRLCGALAGF1
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                                                                                                                                                                                                                                                                                                     LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                                                                                                       2; Indels
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                                                                                                                 Score 2887; DB 5;
Pred. No. 3.5e-234;
0; Mismatches 2;
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Identifying a candidate p53 pathway modulators that are useful as targets for therapeutics or for diagnosing cancers associated with defective p53 function, by providing an assay system having a purified IG polypeptide or nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for identifying a candidate p53 pathway modulating agent. The method comprises providing an assay system having a purified IG polypeptide or nucleic acid, or their functionally active fragment or derivative. The method is useful for identifying modulators of the p53 pathway, particularly for identifying agents for treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung cancer or ancer of the ovary) associated with defective p53 function. The identified modulators are useful as targets for novel therapeutics. The method is also useful for disorders associated with defective p53 function. The IG proteins or nucleic acids are useful as modifiers of the p53 pathway, and as therapeutic targets for disorders associated with defective p53 function. This sequence represents a human protein relating to the human IG genes used in the assay for identifying modulators of the p53 pathway of the invention
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Pred. No. 3.5e-234;
0; Mismatches 2;
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                                                                                                                                                                                                                                            Belvin M,
                                           2001US-0296076P.
2001US-0328605P.
2001US-0338733P.
2002US-0357253P.
2002US-0357600P.
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2002WO-US017313
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nes 547; Conservative
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                                                                                                                                                                                           (EXEL-) EXELIXIS INC
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                                                                  10-OCT-2001;
22-OCT-2001;
15-FEB-2002;
03-JUN-2002;
                                                                                                                                        15-FEB-2002;
                                                05-JUN-2001;
                                                                                                                                                                                                                                                                 Lioubin MN;
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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosing prostatic cancer cancer biggnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosing of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 3000, that binds to the polypeptide; an optymential antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymorleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected
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                             LIRKOYLEEPEKTQWNNVENLNRFERPMDYXEDLKWGMKFVSDEHYDENEDDLVSHVDGS
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                                                                                                                       LIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKWGMKFVSDEHYDENEDDLVSHVDGS
VLAGI FCYRRRTFRGDYFAKNY I PPSDMOKESO I DVLQQDELDSYPDSVKKENKNPVNN
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14-MAY-2003; 2003DE-01022134.
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ROSENTHAL A.
HERMANN K.
PILARSKY C.
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by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 mutine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish proxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polymocleotide and polypeptide sequences used in the method of the
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differential expression analysis.
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Matches 547; Conservative
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Human, nectin-3alpha, therapy, cell adhesion, cell proliferation, sepsis, paracellular transport disorder, kidney, diabetic retinopathy, allergy, allograft rejection; meteataals, restenosis, inflammatory, bowel disease, oedema, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, tumour; cancer, herpesvirus infection, chromosome 3; asthma.
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                                                 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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N-PSDB; AAD37440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection consubstances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide, an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the colypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer prostope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concert patients, or subjects at risk, were incubated prostatic cancer patients, or subjects at risk, were incubated sequencially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish caroningly but non-mailagnent ealls only weakly. In 15 of 63 samples were counterstained with hemalum (blue). Malignant cells stained sequences used in the method of the
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nann H, Roepcke S;
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), Bruemmendorf T, Kinnemann H,
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14-MAY-2003; 2003DE-01022134.
                                                                                                                                    22-FEB-2004; 2004WO-DE000433.
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Beckmann (
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ROSENTHAL A.
HERMANN K.
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                                            WO2004076614-A2.
Homo sapiens.
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Xinzhong L,
                                                                                        10-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                             Hinzmann B,
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                                                                                                                                                                                                                                                                              (DAHL/)
(ROSE/)
(HERM/)
                                                                                                                                                                                                                                                      (HINZ/)
                                                                                                                                                                                                                                                                                                                                                   (PILA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agents.
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8 셤 ò cytostatic; gene therapy; cancer;

immunosuppressant;

Human polypeptide SEQ ID NO 2288.

(first entry)

22-OCT-2001

AAM39143;

peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; any any appropriate the system of the screening; arthritis; inflammation;

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gamma and nection-4 polypeptides and their corresponding polymucleotides.

Certia DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding polymucleotides.

Cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above competing asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, stroke, restenosis, tumour growth and treating endothelial migration.

Continis also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell, (vascular smooth muscle cell). The present sequence is human nectin-Jalpha protein containing 7 amino acids deleted from the N-terminal end. Human nectin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCV 240
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                     invention relates to a substantially purified nectin3alpha,
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100.0%; Pred. No. 2e-232;
iive 0; Mismatches 0;
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Matches 542; Conservative
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23-DEC-1999; 99US-00471275. 25-APR-2000; 2000US-00488725. 25-APR-2000; 2000US-0055217. 20-UN-2000; 2000US-0055317. 19-JUL-2000; 2000US-0059312. 03-AUG-2000; 2000US-0065312. 14-SEP-2000; 2000US-0065315.

26-DEC-2000; 2000WO-US034263

WO200153312-A1 Homo sapiens.

leukaemia.

26-JUL-2001

19-OCT-2000; 2000US-00693036 29-NOV-2000; 2000US-00727344

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymotleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as as peripheral nervous injuries, peripheral nervous as system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWGKONVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
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Zhang J,
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Pred. No. 1.4e-231;
0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 2288; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous system injuries.
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nes 540; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 555 AA;
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Zhou P,
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YV 549 542 -\$

488 481 548 541

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AAM39143 standard; protein; 555 AA.

AAM39143 ID AAM3 XX RESULT 7

EEPEKTOWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREW 547

YRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYL

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Gaps

; 0

9 9 180 180 240

240 300 300 360 360 420 420 480 480 540

540

cancer.

120 120

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and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                               KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQKVIYISDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILAGVFCYRRRRTFRGDYFAKNYI PPSDMQKESQI DVLHQDELDSYPDSVKKENKNPVNN
                                                                                                                                                                                      TTTLQPTVQWHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGGALFLVLVS
                                                                                                                                            MARTPGPAPLCPGGGKAQLSSAFPPAAGLLLPAPTPPPLLLLLIPLLFSRLCGALAGSI
                                                                                                                                                                        IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGE
                                                                                                                                                                                                                    VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDS
                                                                                                                                                                                                                                  VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                                                                                                                               1 MARTPGPSFLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                                                                                                             TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell infiltration; cancer metastasis;
                                                                                                           Indels
                                                                                       Length
                                                                                       1e-221;
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                                                                                     ; Score 2739; Di
; Pred. No. 1e-2:
19; Mismatches
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                                                                                     94.3%;
93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                            Conservative
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                                                                  Sequence 549
                                                                                               Best Local Simi
Matches 512;
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                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic
                                                                          KHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLD
 VWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL
                     NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET
                                 VAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVV
                                                                                                        KHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLD
                                                                                                                                                   GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQRVIYISDPPTTTLQPTI
                                                                                                                                                               QWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCY
                                                                                                                                                                                                         RRRRIFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYLE
                                                                                                                                                                                                                                                    EPEKTOWNIVENLINR PER PMD YY EDLKMGMK FV SDEHYDENEDDLV SHVDGS VISRREWY
                                                                                                                                                                                                                                                                                                adhesion; cell infiltration; cancer metastasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine
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N-PSDB; AAH78179.
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                                                                                                                                                                                                                                                                                                                                                                                              is an immunoglobulin-like coll adhesion molecule that shows homophilic and heterophilic cell-cell adhesion molecule that shows homophilic polymucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a murine nectin-3 polypeptide. Nectin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MARTPGPAPLCPGGGKAQLSSAFPPAAGLILPATPPPLILILIPLILIFSRLCGALAGSI
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                                                                                                                                                                                                                                         or diagnosing and treating tumor infiltration and the mouse nectin-3 protein families and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.3%; Score 2739; DB 4; Length 549; 93.3%; Pred. No. 1e-221;
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                                                                                                                    Sato K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19, Mismatches
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 56-61; 64pp; Japanese.
                                                                                                                    Nakanishi H,
                                        JAPAN SCI & TECHNOLOGY CORP
TAKAHASHI K.
09-MAR-2000; 2000JP-00065595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 93.3
Matches 512; Conservative
                                                                                                                                                                                                                                                                                         corresponding antibodies.
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                                                                                                                    Takai Y,
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                                                                                                                                                                    WPI; 2001-570771/64
                                                                                                                                                                                                                                           protein family
                                                                                                                                                                                        N-PSDB; AAH78182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 549 AA;
                                                                                                                       rakahashi K,
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                                                                      (TAKA/)
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The invention relates to a substantially purified nectinialpha, beta,

C gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with

C cell adhesion activity, adherens juuction formation activity, epithelial

C or endothelial barrier function activity, endothelial proliferation or

migration activity, viral polypeptide binding activity. The epithelial or

c endothelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

c andothelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

c archma, allergy, allograft rejection, metastasis of cancer cells,

paracellular transport disorders such as magnesium transport defects in

the kidney or inflammatory bowel disease. Nectin DNA is also useful for

c inhibiting angiogenesis in a mammal and treating endothelial migration,

proliferation or angiogenic condition of a tissue or a subject, such as

c ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

c stroke, restenosis, tumour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an

c endothelial cell, an epithelial cell or a smooth muscle cell (vascular

c smooth muscle cell). The present sequence is mouse nectin-Jabpha protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                    Mouse; nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR 120
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AAE23291 standard; protein; 549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000; 2000US-0238557P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2001; 2001WO-US031392
                                                                                                                               Mouse nectin-3alpha protein
                                                                                     (first entry)
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nes 512; Conservative
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                                                                                       27-AUG-2002
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RESULT 10 AAE23291

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us-09-972-268-4.rag

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymocleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous containing a polypeptide or polymucleotide of system, such as peripheral nervous system diseases, such as alzeral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, archer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contained the contained and inflammation, leukaemias and contained the contained and inflammation, leukaemias and contained the contained contained the contained contained the contained contai
            treating disorders such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 VSVLA-GIFCYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
              nucleic acids and polypeptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                      Score 2568.5; DB 4
Pred. No. 2.6e-207;
4; Mismatches 33;
                                                              Example 2; SEQ ID NO 5860; 10078pp; English.
                               central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                      part of the printed specification
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91.3%;
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Best Local Similarity 91.3'
Matches 504; Conservative
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, Zhao (
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              LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPPTRFAR
                                 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                               GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT
                                                                                                                                                                 TTTLOPTIONHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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Zhang J,
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Yang Y,
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ΑJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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2000US-00488725.
2000US-00552317.
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25-APR-2000, 2000US-00552317
20-JUN-2000, 2000US-00598042
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03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
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2000US-00727344
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29-NOV-2000;
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LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF

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1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 61 IVEPHVTAVWGKNVSLKCLIEVNETITOISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 300 360

GRRITCVVXHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPF

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KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360

TITLOPIIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 404

KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT

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Gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adhesens junction formation activity, epithelial corresponding barrier function activity, endothelial proliferation or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopath, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, corresponding angiogenesis in a mammal and treating endothelial migration, inhibiting angiogenesis in a mammal and treating endothelial migration, corresponding or inhibiting or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis is a mammal and treating endothelial migration, stochsemia, atherosclerosis, isochaemia-reperfusion injury, thrombosis, stock, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                              Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
                                                                                                                                  paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammacory bowel disease; oedema; atherosclerosis; isothaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 2138; DB 5; Length 426; 100.0%; Pred. No. 3.4e-171; ive 0; Mismatches 0; Indels (
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/note= "Human nectin-3alpha protein"

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                                                                          Human nectin-3alpha-FLAGpolyHis fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                     405. .420
/note= "FLAG peptide"
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                                                                                                                                                                                                                                 Homo sapiens
Unidentified
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AAE23289;
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Human, nectin-Jalpha, therapy, cell adhesion, cell proliferation, sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy, allograft rejection; metastasis, restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia reperfusion injury; thrombosis; gtroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a substantially purified nectin3alpha, beta, agamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Youakim A;
Human nectin-3alpha-IgG1Fc region fusion protein.
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                                                                                     AAE23287 standard; protein;
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1 MARTPGPSPLCPGGGKAQLSSASLIGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGFI

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al Similarity 100.

Query Match

Best Local Matches 40

Region

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migration activity, viral polypeptide binding activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell for modulating proliferation or migration of an smooth muscle cell, The present sequence is a fusion protein containing human nectin-Jalpha protein fused to immunoglobulin IgGl Fc region
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Sequence 634 AA;

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                                                                                                                    IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                         VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                          1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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 DB 5; Length 634;
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                Pred. No. 6.2e-171;
73.6%; Score 2138; D
100.0%; Pred. No. 6.2
ive 0; Mismatches
                           Matches 404; Conservative
               Similarity
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Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemma-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromsome 3.
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                                                                                                                                     AAE23285 standard; protein; 510
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Mus musculus.
Chimeric.
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RESULT 14
                                                                      AAB23385
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Location/Qualifiers

120

9 9 180

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Gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, is considered or a subject, such as stroke, restenosis, tumour growth and treating herpsevirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular muscle cell). The present sequence is a fusion protein encoding amino acids from mouse nectin-3 protein and the rest form human nectin-
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3beta protein. Human nectin-3beta gene is located on chromosome 3.
(Updated on 29-AUG-2003 to standardise OS field)
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/note= "Human nectin-3beta protein"
1. .6
/note= "Mouse nectin-3 pprotein"
7. .510
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paracellular transport disorders such as magnesium transport defects in the kidney or infilammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in ammmal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as stroke, restenosis, ischemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an amothelial cell, an egithelial cell or a smooth muscle cell, wascular smooth muscle cell). The present sequence is a fusion protein containing human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
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glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

Claim 9; Page 102-104; 141pp; English.

sepsis, stroke.

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                                        Gaps
                                        32;
Length 595;
                                      Indels
                                          70;
65.6%; Score 1907; DB 5; 76.4%; Pred. No. 1.7e-151; ive 16; Mismatches 70;
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Query Match
Best Local Similarity 76.49
Matches 383; Conservative
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ne : 94.6763 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1
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Run on:

October 6, 2005, 09:42:42; Search time 18.0493 Seconds (without alignments) 2926.593 Million cell updates/sec

Title: Perfect score:

US-09-972-268-4 2905 1 MARTPGPSPLCPGGGKAQLS..........EDDLVSHVDGSVISRREWYV 549 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	re		poliovirus recepto		PRR2 delta - human	poliovirus recepto	poliovirus recepto			colon carcinoma-as	irregular chiasm C	perlecan precursor	hypothetical prote	hemicentin precurs	adhesion molecule	surface glycoprote	neural cell adhesi	OX-2 membrane glyc	elastic titin - hu	DM-GRASP precursor	Down syndrome cell	heparan sulfate pr	B-cell adhesion pr	cell adhe	neural cell adhesi	myelin-associated	SHP substrate-1 pr	fibroblast growth
SUMMARIES		32	24	P3	37	9	93	94	94	PD	PA	17	48	96	92	90	90	54	NC	39	46	64	51	52	71	NC	NG	85	68	51
Ø	Ð	087	JC4024	HL,MSP3	A53437	153960	168093	A44194	B44194	RWHUPD	RWHUPA	A54017	A49448	A38096	T20992	T43290	JH0506	A45254	IJBONC	A47639	138346	JH0464	T08851	S18252	JH0371	IJRTNC	IJHONG	B3378	JC528	B491
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d	Query Match	73.7	21.6	17.0	16.2	16.0	15.5	14.5	14.3	13.4	13.4	11.4	7.9	7.4	6.9	6.9	6.8		6.5	6.5	•	•	٠	6.2	٠	6.0	9.0	9.0	o. 0	5.9
	Score	2141	627	494	470	463.5	449.5	422.5	415.5	390.5	390.5	331.5	230.5	215.5	201	201	198	194	189	187.5	187.5	182	181.5	179	178.5	174	173.5	173	7	171.5
	Result No.		7	m	4	S	9	7	80	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 JC4024

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	30 31 32	33 34 35	36 337 38	39 41 41	4 4 4 2 6 4	45

ALIGNMENTS

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Reference number: A38211; MUID:92219365; PMID:1560525
                          A;Accession: A38213
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(Species: Mus musculus domesticus (western European house mouse)
(5)Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
(5)Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
                                                                                                                                                        A Accession: UC4024
A, Molecule type: mRNA
A, Residues: 1-518 < LOP>
A, Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C; Genetics:
A, Gene: GDB:PVR1
A, Cross-references: GDB:583951
A, Map position: 11q23-11q24
C; Superfamily: poliovirus receptor; immunoglobulin homology
C; Keywords: glycoprotein; transmembrane protein
F; 1-30/Domain: signal sequence #status predicted <SIG>
F; 1-30/Domain: ransmembrane #status predicted <TMN>
F; 31-519/Domain: transmembrane #status predicted <TMN>
F; 356-779/Domain: transmembrane #status predicted <TMN>
F; 36, 72, 82, 139, 287, 308, 333/Binding site: carbohydrate (Asn) (covalent) #status predicted
poliovirus receptor-related protein precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JG4024
R;Lopez, M; Eberle, F; Mattei, M.G; Gabert, J.; Birg, F; Bardin, F; Maroc, C.; Dubz A;Lopez, Z61-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene A;Reference number: JG4024; MUID:95237621; PMID:7721102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
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ILLVLI-VVGGIVVALRRRRHTFKGDYSTKKHVYGNGYSKAGIPQHHPP--MAQNLQ--- 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6%; Score 627; DB 2; Length 518; 30.8%; Pred. No. 3.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 30.89
Matches 164; Conservative
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C.Date: 06-Oct.1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A53437
R.Acki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
T. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with pc
A;Reference number: A53437; MUID:94179228; PMID:8132569
                                                                                                                                    PIDN: AAA39734.1; PID:g199786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 SFEEPILLPVTLSVRYPPEVSISGYDDNWYLGRSEAILTCDVRSNPEPTDYDWSTTSGVF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQMH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- FGNGG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;355-374/Domain: transmembrane #status predicted <TMN>
F;375-467/Domain: intracellular #status predicted <TMT>
F:54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VLPPSRLSPTLPLLPLLLLLQETGAQDVRVRVLPBVRGRLGGTVELPCHLLPPTTERVS
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A; Molecule type: DNA
A; Residues: 1-467 < MOR>
A; Residues: 1-467 < MOR>
A; Residues: 1-467 < MOR>
A; Cross-references: UNIPROT: P32507; GB: M80206; NID: 9199785; PIDN: AAA35
C; Superfamily: poliovirus receptor; immunoglobulin homology
C; Keywords: duplication; glycoprotein; transmembrane protein
F; 25-450 Fomain: signal sequence #status predicted < SIG>
F; 26-467/Product: poliovirus receptor homolog #status predicted < MAT>
F; 26-134/Domain: immunoglobulin homology < IMM1>
F; 167-231/Domain: immunoglobulin homology < IMM3>
F; 267-322/Domain: immunoglobulin ho
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al Similarity 27.4%; Pred. No. 1.1e-27;
153; Conservative 69; Mismatches 201;
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C;Accession: 168093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Rane 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th A;Reference number: I53960; WUID:95347610; PMID:7622062
A;Accession: 168093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYED 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRR2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                         13 PPTP----LLWPLLLLLLLETGAODVRVQVLPEVRGOLGGTVELPCHLLPPVPGLYISL
                                                                                                                                                                                                               ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF------KNYSLNDATITL
                                                                                                                                                                                                                                                                                               HNIGPSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNET
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                                                                                                                                                                                                                                                                                                                                                                               189 VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 TLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 PPTPPPLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI----EVNETITQ
                                                                                          Gaps
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A;Residues: 1-538 <RES>
A;Cross-references: UNIPROT:092692; GB:S79172; NID:g1042204; PID:g1042205
C;Genetics:
                                                                                        Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 135;
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                                               Ouery Match 16.0%; Score 463.5; DB 2; Best Local Similarity 25.5%; Pred. No. 1.8e-25; Matches 147; Conservative 76; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 LKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 549
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15.5%; Score 449.5; DB 2;
Best Local Similarity 24.6%; Pred. No. 2.1e-24;
Matches 139; Conservative 91; Mismatches 200;
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        F;276-331/Domain: immunoglobulin homology <IMM>
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C; Superfamily: pol
F; 276-331/Domain:
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A;Accession: A53437
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-530 <AOK>
A;Cross-references: UNIPROT:P92507; GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A;Experimental source: C57/Baic, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IWM>
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C;Species: Homo mappiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 153960
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                       295 PASAVAQGSQL-LVHSVDRMVNTTFICTATNAVGTGRAEQVILVRESPSTAGAGAT--- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :: | | | : | : | : | : | : | CORKEORLOAADEEEELEG---PPSYKPPTPKAK-----LEEPEMPSQLFTLGASEHSP 425
                                                                                                                                                                                                                                                                                                                                                                             QISWEKIHGKSSOTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQW 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAG---IFCY 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                             30 LLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT 87
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                         Query Match
16.2%; Score 470; DB 2; Length 530;
Best Local Similarity 24.8%; Pred. No. 7.1e-26;
Matches 140; Conservative 90; Mismatches 212; Indels 122;
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C;Superfamily: poliovirus receptor; immunoglobulin homology
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A; Residues: 1-478 < RES>
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A;Reference number: A44194; MUID:93059651; PMID:1331508
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                                                                                                                                                                                   383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDYFAKNY 443
                   263
                                                                                                                           PKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRR--RTF----- 434
                                                                                                                                                                                                                                                                                       WEKIHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEGDLGEMESTITS--FPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL 263
                                                                                                DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PPLLLLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQIS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKAVTPPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID
                                                                                                                                                                                                      WEGDLGEMESTITS--FPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL
                                          179 WHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFEKPQLLTVNL
                                                                                                                                                                                   324 FVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATE
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C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 415.5; DB 2; 28.1%; Pred. No. 3.8e-22; ive 72; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                             382 PSSEEHASASANGYISYSDVSREA 405
                                                                                                                                                                                                                                                                                                                                                   ----RGDYFAKNYIPPSDMQKES 453
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A;Molecule type: DNA
A;Residues: 1-392 <KOI>
                     206
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A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Species: Cercopithecus acthiops (green monkey, grivet)
C;Species: Cercopithecus acthiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44194
R;Koike, S; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta A;Reference number: A44194
A;Reference number: A44194
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEKIHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A--GIFCYRRRR---TFRGDYFAK-----NYIPPSDMQKESQIDVLQQDELDSYPDSVK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGILICRQQRKEQTLQGAEEDEDLEGPPSYKPPTPKAK----LEAQEMPSOLFTLG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                        -- KNYSLNDATITL 135
                                                                  ::|:: :: | || || : | || ||: | VIWORPDAPANHONVAAFHPKMGPSFPSPKPGSERLSFVSAKOSTGODTEAELODATLAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GGIIGGIIAAIIATAV 374
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67
                                                                                                                                                     | : | | | : | | | : | | | | HICLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQABAQKVTFSQDP-----T
                                                                                                                                                                                                                                               179 TVALCISKEGRPPARISWLSSLDWBAKETQVSGTLAG----TVTVTSRFTLVPSGRADGV
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PPTP-----LLWPLLLLLLLTGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL
                                                                                                                         HNIGFSDSGKYICKAVTPPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNET
                                                                                                                                                                                                          VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                       RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS
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A;Cross-references: UNIPROT:P32506; GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology C;Keywords: transmembrane protein
C;Keywords: immunodlobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Mismatches 175;
                                          ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF-
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Best Local Simil
Matches 126; C
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: 312048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA454
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A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble for
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A;Cross-references: GDB:120324; OMIM:173850
A;Genes. GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Cross-references: GDB:12032-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q13.2-19q1
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F$88-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: the gamma form has 331-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and A;Reference number: A90910; WUID:89168426; PMID:2538245
A;Accession: A31496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
     333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK
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                                                                                                                                                         - PSEHSGMSR-----NAIIFLVLGILVFLILLGI--GIYFY 366
                                                                                                 387 LPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCY
                                                                                                                                                                                                                                                                                                                                                                                                                               poliovirus receptor splice form alpha precursor - human N;Alternate names: poliovirus receptor H201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 390.5; DB 1; 27.6%; Pred. No. 2.6e-20; ive 68; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fi159-223/Domain: immunoglobulin homology <IMM2>F;259-314/Domain: immunoglobulin homology <IMM3>
301 PVDKPINTTLICNVTNALGARQAELTVQVKEGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: poliovirus receptor H20A N;Contains: poliovirus receptor beta
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Best Local Similarity 27.6*
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: 67-Ala was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                                                                                                                                                                                       RAHUDD

POLIOVIUS FREEDELS

RAHUDD

POLIOVIUS receptor splice form delta precursor - human

NiAlternate names: poliovius receptor H20B

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: A43024, B31496

R;Koike, S; Horie, H; Ise, I; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

R;Koike, S; Horie, H; Ise, I; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

R;Koike, S; Horie, H; Ise, I; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

R;Koike, S; Horie, H; Ise, I S; PMID:2170108

A;Accession: A33024

A;Molecule type: DNA

A;Residues: 1-392 - KOI->

A;Note: 67-Ala was also found

R;Mondelsohn, C.L.; Wimmer, E.; Racaniello, V.R.

Cell 56, 855-865, 1889

A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e

A;Accession: B31496

A;Accession: B31496
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C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
E;1-20/Domain: signal sequence #status predicted <SIG>
F;1-39/Product: poliovirus receptor delta #status predicted <MAT>
F;21-343/Pomain: extracellular #status predicted <EXT>
F;21-325/Domain: immunoglobulin homology <IMMI>
F;159-223/Domain: immunoglobulin homology <IMMI>
F;259-314/Domain: immunoglobulin homology <IMMI>
F;250-314/Domain: immunoglobulin homology <IMMI>
F;250-314/Domain
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F;368-392/Domain: intracellular #status predicted <1MT>
F;49-123.166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 YPPEVSISGYDNNWYLGQNEATLICDARSNPEPIGYNWSTIMGPLPPFAVAQGAQL-LIR 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 PLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 VIFPQGSRSVDIWLRVLAKPONTABVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1
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A;Residues: 1-66,'A',68-392 <MEN>
A;Cross-references: GB:M24406
380 LSPSSEHHQS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: PVR; PVS
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267 YAPEVSYTGYDGNWFVGRKGVNLKCNADANPPPFKSYWSRLDGQW	RESULT 12 A49448 irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster) N;Alternate names: irreC-roughest protein C;Species: Drosophila melanogaster C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004 C;Accession: A49448; S34129 R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandste
Oy 387 LPFPLSTLATIKDDTTATIASVVGGALFIVUVSVLADIFCY 428	Genes Dev. 7, 2533-2547, 1993-32467, 1995 A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal projec A;Reference number: A49448; MUID:94102535; PMID:7503814 A;Accession: A49448
RESULT 11 A54017 colon carcinoma-associated antigen pB4 precursor - rat N/Alternate names: pB4 protein C;Species: Rattus norvegicus (Norway rat) C;Decies: Rattus Asquence_revision 02-Aug-1994 #text_change 09-Jul-2004 C;Accession: A54017; A61206	A; Molecule type: DNA; mRNA A; Residues: 1-764 <ram> A; Residues: 1-764 <ram> A; Cross-references: UNIPROT:Q08180; GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NII C; Genetics: A; Gene: FlyBase:rst A; Cross-references: FlyBase:FBgn0003285 C; Keywords: transmembrane protein</ram></ram>
R;Chadeneau, C.; LeMoullac, B.; Denis, M.G. J. Biol. Chem. 269, 15601-15605, 1994 A.Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinom A;Reference number: A54017; MUID:94253144; PMID:8195207	Query Match 7.9%; Score 230.5; DB 2; Length 764; Best Local Similarity 19.4%; Pred. No. 1.88-08; Matches 118; Conservative 87; Mismatches 177; Indels 227; Gaps 26;
A;Accesion: A54017 A;Actus: pre-liminary A;Molecule type: mRNA A;Residues: 1-416 < CHA>	Qy 40 LLLLFPLLLFSRLCGAL-AGPIIVEPH-VTAVWGKNVSLKCLIEVNETITQ1 89 :
A;Cross-references: UNIPROT:Q7M048; GB:L12025 R;Chadeneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K. Int. J. Cancer 47, 903-908, 1991 A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcin	QY 90 SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDS 143
A;Reference number: A61206; MUID:91184910; PMID:2010233 A;Accesation: A61206 A;Molecule type: protein A;Residues: 34-41,'X',43-53 <ch2></ch2>	Qy 144 GKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKP 200
A;Note: the residue at position 9 is suggested to be glycosylated asparagine C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cel C;Keywords: glycoprotein; membrane protein	QY 201 VAHIDWEGDLGEMESTTTSFPNETA-TIISQYKLPPTRFARGRRITCVVKHPALE 254
Query Match 11.4%; Score 331.5; DB 2; Length 416; Best Local Similarity 28.1%; Pred. No. 4.4e-16; Matches 104; Conservative 56; Mismatches 171; Indels 39; Gaps 12;	
Qy 8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLFPLLLFSRLCGALAGPIIVEPHVT 67	290 KCNADANDPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVXI-CKVTNSLGGRS
QY 68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF-K 124	349 DQKVIXISDPRTTTTLQPTIQW-HPS
QY 125 NY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSL 181	374TADIBDLATEP 374TADIBDLATEP 3.04 GOVENNYANDENYANTERANANINY KOCBATOCOPHONY INDIBATEP
QY 182 IDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTR 237 :	385 KKTI 385 KKTI 385 KKTI 385 KKTI
QY 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297	403ATIIASVVGGALFIVLVSVLAGIFCYRRRFFRGDYFAKNYIPP
QY 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSG-VYICKVTNSLGQRSDQKVIYIS 356	A A T A T A T A T A T A T A T A T A T A
Oy 357 DPPTT 361 Db 339 EASELLPPKT 348	50/ ADVISSOU. SULT 13 8096 Flecan precursor - hum

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Gaps

Indels 115;

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A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1
       F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;156-16(0)Comain: laminin-type EGF-like homology <EG7>
F;156-16(0)Comain: laminin-type EGF-like homology <EG7>
F;1677-3666/Domain: laminin-type EGF-like homology <LEG8>
F;1677-3666/Domain: IV <LOW4>
F;2007-2014/Domain: IV <LOW4>
F;3007-2014/Domain: EGF homology <EG7>
F;3867-3800/Domain: EGF homology <EG7>
F;388-3921/Domain: EGF homology <EG7>
F;388-3921/Domain: EGF homology <EG7>
F;4147-4175/Domain: EGF homology <EG72>
F;4147-4175/Domain: EGF homology <EG72>
F;4149-4151/Region: motor neuron attachment (L.R.E) motif F;6571,776/Einding site: heparan sulfate (Ser) (covalent) #status predicted F;65,71,76/Einding site: heparan sulfate (Ser) (covalent) #status predicted F;89,554,1755,2121,3072,3105,3379,3780,3836,4068/Einding site: carbohydrate (Asn) (cov. F;295,393,4179/Einding site: chondroitin sulfate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2884 SPADSGEYSCQVTGSSGTLEASVLVTIEPSSPGPI-------PAPGLAOPIYIEA 2931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3025 S-IDPPSSTVQQQQD-ASFKCLIHDGAAPISLEWKTRNQELEDNVHISPN--GSIII--- 3077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYK 232
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20992; T24733
St;Sulston, J.
Submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADANPPPFKSVWSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 215.5; DB 2; Length 4391; 2.9%; Pred. No. 2.7e-06; ve 63; Mismatches 165; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTV-
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A;Molecule type: DNA
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A;Reference number: 219929
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Best Local Similarity 22.9%
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD proteil adhesion molecules, and epidermal growth factor.

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD proteil adhesion molecules, and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768

A;Rolecule type: mRNA

A;Residues: 1-57, D', 59-434, A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R'
71-2979, 'H', 2901-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3

A;Cross-references: BMBL:X62515

R;Tryggvason, K.
submitted to the EMBL Data Library, October 1991

A;Reference number: S77946

A;Rocession: S77946

A;Rocession: S77946

A;Ross-references: BMBL:X62515; NID:292469; PID:CA444373.1; PID:G29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.
Genomics 11, 389-396, 1991

A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the ghacenession: A41059

A;Reference number: A41059; MUID:92120660; PMID:1685141

A;Reference number: A41059
NyAlternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote C; Species: Homo sapiens (man)
C; Saccession: A38096; S19256; S77946; A41059; A40306; B33525; A33625; A41736
R; Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 844-8557, 1992
A; Title: Primary structure of the human heparan sulfate proteoglycan from basement membr tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A; Reference number: A38096; MUD:92235084; PMID:1569102
A; Accession: A38096
A; Molecule type: mRNA
A; Residues: 1-4391 < MUR.
A; Residues: 1-4391 < MUR.
A; Residues: 1-4391 < MUR.
A; Cross-references: UNIPROT: P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
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A; Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD>
A; Cross-references: GB: M46283; NID: g184424; PIDN: AAAS2699.1; PID: g184425
R; Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 109, 3199-3211, 1989
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C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembra
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F;199-234/Domain: LDL receptor ligand-binding repeat homology F;285-319/Domain: LDL receptor ligand-binding repeat homology F;325-359/Domain: LDL receptor ligand-binding repeat homology F;368-403/Domain: LDL receptor ligand-binding repeat homology F;531-1676/Domain: LDL receptor ligand-binding repeat homology
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A;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>
A;Note: peptide potentially matches four different regions
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A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
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A; Residues: 1-5198 <WI2>
A; Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FISG9.4b
A; Experimental source: clone T09B9
C; Genetics:
A; Gen
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A,Molecule type: DNA
A,Residues: 1-5175 <W12>
A,Residues: 1-5175 <W12>
A,Festidues: 1-5175 <W12>
A,Experimental source: clone T09B9
C,Genetics:
A,Gene: CESP:F15G9.4a
A,Gene: CESP:F15G9.4a
A,Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2533/3; 2699/3; 2759/1; 485/1; 4879/1; 4879/1; 5011/1; 5077/1; 5011/1; 5077/1; 5011/1; 5077/1; 4225/1; 4361/1; 4361/1; 456/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 5077/1; 507
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hemicentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: Il-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: Il-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43290; T20993; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and c;A;Reference number: Z22396
A;Accession: T43290
A;Access
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A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
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A;Residues: 1-5198 <VOG>
R;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulaton, J.
submitted to the EMBL Data Library, December 1994
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A;Accession: T20993
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Kershaw, J.
submitted to the EMBL Data Library,
A;Reference number: Z19929
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                                                                                                                                                             Gaps
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      Length 5198;
Query Match 6.9%; Score 201; DB 2; Length 51 Best Local Similarity 25.4%; Pred. No. 3.7e-05; Matches 100; Conservative 50; Mismatches 156; Indels
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Query Match
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P32506 cercopithec		Q63611 rattus norv	Q08835 cercopithec	_	Q8hy14 oryctolagus	Q8k094 m hypotheti	P15151 homo sapien	Q8bvf6 mus musculu	Q8hy15 lemur catta	Q60977 mus musculu	Q6ayp5 rattus norv	Q8r5m8 mus musculu	Q9by67 homo sapien
PVR CERAE	Q9RĪE1	063611	Q08835	Q91WP1	Q8HY14	Q8K094	PVR HUMAN	QBBVF6	Q8HY15	060977	Q6AYP5	QBR5MB	Q9BY67
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417	412	412	401	408	412	408	417	408	403	415	476	456	442
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14.	1,4	Н	_										
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606,
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 1.
SMART; SMO4099; IG; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;
                                                                    Last sequence update)
Last annotation update)
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Pred. No. 5.2e-207;
0; Mismatches 2;
549 AA
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PRT;
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                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6
Matches 547; Conservative
PRELIMINARY;
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610301B19 product:poliovirus receptor-related
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                              241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                   GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF
                                                                                                     KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT
                                                                                                                                                                                                          361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
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STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meth. Enzymol. 303:19-44(1999)
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 full insert sequence.
Name=Pvrl3;

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                                TTTLQPTIQMHPSTADIEDLATEPKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVS
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     TTTLQPT1QWHPSTAD1EDLATEPKKLPFPLSTLAT1KDDT1AT11ASVVGGALF1VLVS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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549 AA; 60582 MW; 5492C9ABB472F185 CRC64;
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J. Biol. Chem. 275:10291-10299 (2000).
M. Biol. Chem. 275:10291-10299 (2000).
M. MOJ. MAF195833; AAF63685.1; -.
M. MOJ. MOJ. 1930171; Pvrl3.
G. GO:0005813; C:cell.-cell adherens junction; IDA.
GO; GO:0005815; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0015515; F:protein binding; IPI.
GO; GO:0016317; P:coll-cell adhesion; IDA.
InterPro; IPR003299; IG.
InterPro; IPR003110; IG-like.
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Last annotation update)
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Name=Pvrl3;
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93.3%;
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Matches 512; Conservative
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01-MAR-2004 (TrEMBLrel.
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                                                                                                                                  LIRKDYLEEPEKTOWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
      TTTLQPTVQWHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGGALFLVLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%; Score 2141; DB 2; Length 407; 99.3%; Pred. No. 1.9e-151; ive 1; Mismatches 2; Indels (
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J. Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL050071; CAB43256.1; -. PIR; T08732; T08732. InterPro: IRR07110; Ig-like. PROSITE; PS50835; IG LIKE; 2. Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp5566B0846 (Fragment).
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Matches 404; Conservative
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TISSUE=Kidney;
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukuda Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukuda T., Hori F.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konoh H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Nomo H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Nomo H., Kouda M., Koya S., Kurihara C.,
A Rasuki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Saski D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sano H., Saski D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagawi M., Tagawa A., Takahashi F., Tanaka T.,
A Pejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BND: MGJ: 1930171; Pvrl3.
CG): GO:0005515; C:cell-cell adherens junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
CG): GO:0016337; Precellular space; TAS.
CG): GO:0016337; C:mtegral to membrane; TAS.
CG): GO:001647; C:mtegral to membrane; TAS.
CG): GO:001647; C:m
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MAINDER M., Aizawa K., Razawa K., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumamoto R., Matsumco H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumco H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Cogawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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PROSITE; PS50835; IG_LIKE; 3.
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                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Mangner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rah, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IVEPHYTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGBYQGR 120
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC067808; AAH67808.1; -InterPro; IPR003599; IG. InterPro; IPR007110; Ig-11ke.
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 3.
GPOTIENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
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                                                366 AA.
                                                                                                 Created)
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27,
                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 99.2
Matches 353; Conservative
                                                PRELIMINARY;
                                                                                                                        05-JUL-2004 (TrEMBLrel.
                                                                                              05-JUL-2004 (TrEMBLrel).
                                                                                                                                                                                                                       Homo sapiens (Human)
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241 GRRITCVVKHQALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
Satch-Horikawa K., Nakanishi H., Takhhashi K., Miyahara M.,
Tachibana K., Mizoguchi A., Takhasi Y.;
"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                           301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVXICKVTNSLGQRSDQKVIXIS 356
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM0040; 13; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:10291-10299(2000).

EMBL, AF195834; AAF63686.1; -.

MGD; MGI:1330171; Pvr13.

GO; GO:0005913; C:cell-cell adherens junction; IDA.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016317; P:cell-cell adhesion; IDA.

InterPro; IPR003599; IG.

InterPro; IPR003599; IG.
                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) cell adhesion molecule nectin-3 beta.
                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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241 YLEEPEKTQMANVENLARFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRR 300
GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                          -----SSIA----VAGAVIGAVLALFIIT 383
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                                          KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT
                                                                                                                               TTTLQPTIQMHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 FCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                                                                                                                                                                                                                                384 VFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPVYEERIPSLPQKDL 428
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                                                                                                                                                                                                                         421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQQDEL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
NON TER
SEQÜÜENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to nectin 3; DKFZP566B0846 protein (Fragment).
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
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nes 304; Conservative
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TISSUE=Cervix;
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                                            VLAGIFCYRRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQQDEL----DSYPDSVKK 472
                                                                      ENK-----NPVNNLIRKDYLEEPEKT-QWNNVENLNRFERPMDYYEDLKMGMKFVSDEHY 526
  ---VAGAVIGAVLALFIIT 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291; Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M., Tachibana K., Mizoguchi A., Takahashi K., Miyahara M., "Nactin-an K., i i mamber of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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llarity 76.7%; Pred. No. 5.7e-128;
Conservative 25; Mismatches 41; Indels 43;
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SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 275:10291-10299(2000).

EMBL; AF195835; AAF63687.1; -.
MOD; MOI:1930171; PV-13.

GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; F:procein binding; IPI.
GO; GO:0016317; P:cell-cell adhesion; IDA.
InterPro; IPR003199; IG.
InterPro; IPR007110; IG-like.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       438 AA
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                                                                                                                                                                                                                           527 DENEDDLVSHVDGSVISRREWYV 549
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SMART; SM00409; IG; 1.
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358; Conserv
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     QSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 195
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MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
Lecoqu E., Dubreuil P., Campadelli-Fiume G.;
"The murine homolog of human nectin1 delta serves as a species
nonspecific mediator for entry of human and animal alpha herpesviruses
in a pathway independent of detectable binding to gD.";
Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                                                                                                                                                                                                                                                                            QSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT
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                                                                                                                                                                                                                                                                                                                             41 LLLFPLL--LFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS
                                                                               TISSUB-Placenta;

TISSUB-Placenta;

TISSUB-Placenta;

TISSUB-Placenta;

TISSUB-Placenta;

TOCA T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR003599; Ig.

InterPro; IPR00499; IG: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JKF6; Q9ERL5; Q9J117;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                Length 267;
                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                         4F464A8A1BA0C451 CRC64;
       Last annotation update)
                                                                                                                                                                                                                                                                             42.5%; Score 1235; DB 2;
96.0%; Pred. No. 5.4e-84;
tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mediator C) (HveC) (Nectin 1).
Name=Pvrll; Synonyms=HveC, Prrl;
Lévunetical protein FLJ90624.
Homo sapiens (Human).
Eukaryota: Mere
                                                                                                                                                                                                                                                         267 AA; 29253 MW;
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Matches 242; Conservative
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                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Policolinia receptor related protein 1.
Extracellular (Potential).
Cytential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
Poly-Glu.
Poly-Glu.
By similarity.
By similarity.
N-linked (GlcNAc. ..) (Potential).
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PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                      Zhan J., Wimmer E.; "MPRRI", a herpesvirus receptor, is expressed in the
MEDLINE=20541977; PubMed=11090177;
DOI=10.1128/JVI.74.24.11773-11781.2000;
Shukla D., Dal Canton M.C., Rowe C.L., Spear P.G.;
"Striking similarity of murine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-:- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                        floor plate during embryogenesis, suggesting a role in neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFF608EBSFFB7A0F CRC64;
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EMBL; AF270977; AAF76195.1; -.
EMBL; AF270977; AAF76195.1; -.
HSSP, OG5793; 1G14.
MGD; MGI:1926483; Pvrll.
GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; IDA.
InterPro; IPR07110; IG-like.
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N -> D (in Ref. 1).
P -> PP (in Ref. 2)
S -> G (in Ref. 3).
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Pred. No. 1.4e-40;
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                                                                                                                                                                        alphaherpesvirus entry.";
J. Virol. 74:11773-11781(2000).
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57064 MW;
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32.5%;
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                                                                                                                                                                                                                                                                                                       STRAIN=Swiss Webster;
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428
515 AA;
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"Generation and initial
                                                                                                                                  Strausberg R
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18;
                                                                                                                                                                                                                                             243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302
                                                                                                                                                                                                                                                                                                                                   281 HWTTLNGSLEKGVEAQNRTLFFRGPITYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGIF--CYRRRRTFRGDYFAXNYI------PPSDMQKESQIDVLQQDELDSY 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGIIVALRRRRHTFKGDYSTKKHVYGNGYSKAGIPQHHPP--MAQNLQ------Y 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSVKKENK-NPVNNLIRKDYLEBPEKTQWNNVE-------NLNRFER 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDDSDDEKKASPLGG---SSYEBEBEBEGGGGGGRKVGGPHPKYDEDAKRPYFTVDEABA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
                                                                                                                                                       GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                     LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                                                                                                      -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISOYKLFPTRFARGR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
95;
Indels
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Last annotation update)
175;
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83; Mismatches
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STRAIN=C57BL/6; TISSUE=Brain;
Conservative
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OG P9M9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PODSDDEKKAGPLGG---SSYEEEEEEEEGGGGGERKVGGPHPKYDEDAKRPYFTVDEAEA 474
analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 FIDGTIRLSGLELEDEGMYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 SLACIVNY-HLDR-FRESLTLNVQYEPEVTIEGFDGNWYLORTDVKLTCKADANPPATEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.5%; Score 653.5; DB 2; Length 515; 32.3%; Pred. No. 3.9e-40;
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                                                                                                                                                   (NOV-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                      PDSVKKENK-NPVNNLIRKDYLEEPEKTQWNNVE------
                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83; Mismatches 176;
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                                                               [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 2.
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SMART; SM0409; 1G; 2.
SMART; SM00408; 1Gc2; 2.
SMART; SM00406; 1Gc2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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or send an email to license@isb-sib.ch)
                                                                                                                                                         AF196770;
AF196771;
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                                                                                                                  AF196768;
                                                                                                                                         AF196769;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Nat. Genet. 25:427-430 (2000).
-!- PUNCTION: Probably involved in cell adhesion. Receptor for
alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with HSV glycoprotein D (gD).
SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-95237621; Pubmed-7721102; DOI=10.1016/0378-1119(94)00842-G;
LOPEZ M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
Dubreuil P.;
"CDNA characterization and chromosomal localization of a gene related
                                                                                                                                                                                                                                                                                                                                                                                                                       Spear P.G., "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-98279152; PubMed-9616127; DOI=10.1126/science.280.5369.1618;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM GAMMA).

MEDLINE=21256041; PubMed=11356977;

DOD=10.1128/JVT.75.12.5684-5591.2001;

Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,

Campadelli-Fjume G., Dubreuil P.;

Campadelli-Fjume G., Dubreuil P.;

TNOVAL, Soluble isoform of the herpes simplex virus (HSV) receptor nectini (or prri-HIGF-HVec) modulates positively and negatively gusceptibility to her infection.";
                        Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20392396; PubMed=10932188; DOI=10.1038/78119; Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helma J.A., Spritz R.A., Arciding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
      05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q15223-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1 and poliovirus receptor.";
Science 280:1618-1620(1998).
                                                                                                                                                                                                                                                                                                     to the poliovirus receptor gene.";
Gene 155:261-265(1995).
                                                                               Name=PVRL1; Synonyms=HVEC, PRR1;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virol. 75:5684-5691(2001).
                                                                                                                                                           NCBI_TaxID=9606;
                                                               antigen).
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-> KPRPQRCLGSAARLLAGTVAVFLILVAVLTVFFLYNRQ
QKSPPETDGAGTDQPLSQKPEPSPSRQSSIVPEDIQVVHLD
PGRQQQEEEBDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
PGP (in isoform Alpha).
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Extracellular (Potential).
Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like C2-type 1.
Ig-like C2-type 2.
Poly-Glu.
By similarity.
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Missing (In isoform Alpha).
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/FIId=VSP 002624.
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AAG16648.1; JOINED.
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AF196772; AAG16649.1; JOINED.
AF196773; AAG16649.1; JOINED.
CAA53980.2; ALT_INIT
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AF196768; AAG16649.1;
AF196769; AAG16649.1;
AF196770; AAG16649.1;
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                                  GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                           TLOPTIOWHPSTADIEDLATEPKKLPPPLSTLATIKDDTIATITASVVGGALFIVLVSVL 422
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                                                 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
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Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity) SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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-i- FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) ent:
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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larity 31.9%; Pred. No. 7.8e Conservative 80; Mismatches
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Q9GL76;
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use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 LGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIA 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%; Score 641.5; DB 1; Length 515; 32.0%; Pred. No. 3.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Poliovirus receptor related
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BFAB00320DDE3785 CRC64;
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(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Ig-like C2-type 1.
Ig-like C2-type 1.
Ig-like C2-type 2.
Poly-Glu.
Poly-Gly.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
N-linked (GlcNAc.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57047 MW;
                                                                                                                                                                                         EMBL; AF308632; AAG30281.1; -
HSSP; 005793; 1GL4.
                                                                                                                                                                                                                         HSSP; Q05793; 1GL4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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248 ASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYN-WTRLDGPLPSGVRVDGDTLGF-PPL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 VTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDL 210
                                                                                                                                                                                                                                                  271 VSVTGYDGN--WFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPL 328
                                                                                                                                                                                                                                                                                                                                                                     329 TENYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 FPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRRTFRGDYFAKNYIPPSD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 MQKESQIDVLQQDELD-----SYPDSVKKENKNPVNNLIRKDYLEEPEKTQ 494
                                                                                                                                                            188 KGTTSSRSFKHSRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAB
                                                                                                                                                                                                                                                                                                                                                                                                           306 TTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQ------VDLV-----
                                                            130 STFPAGSFQARLRLRVLVPPLPSLNPGP-ALEEGQGLTLAASC-TAEGSPAPSVTWDTEV
                                                                                                                         211 GEMESTITSFPNETATIISQYKLFPIRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: : : : | : | 145 YSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              495 WNNVENLNRFERPMDYY------EDLKMGMKFVSDEHYDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein FLJ14847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 IH-GKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLN--DATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 PPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLI--EVNETITQISWEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21560925; PubMed=11544254; DOI=10.1074/jbc.MI03810200;
Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
"Nectin4/PRR4, a new afadin-associated member of the nectin family that trans-interacts with nectin1/PRR1 through V domain interaction.";
J. Biol. Chem. 276:43205-43215(2001).
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                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
      498 VENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 510;
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Last annotation update)
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Pred. No. 5.9e-32;
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EMBL; BC010423; AAH10423.1; --
InterPro; IPR07110; Ig-like.
Pfam; PF0047; ig; 1.
PROSITE; PSS0835; IG LIKE; 3.
SEQUENCE 510 AA; 55454 MW; D
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                                                                                                                                                                                                                                                                                                                36 PPPLILLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLI--EVNETITQISWEK 93
                                                                                                                                                                                                                                                                                                                                         12 PEAWLLILLILASFTGRCP--AGELGTSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWAR 69
"Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                   Query Match
18.7%; Score 543; DB 2; Length 510;
Best Local Similarity 28.4%; Pred. No. 7e-32;
Matches 149; Conservative 85; Mismatches 213; Indels
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                                Nat. Genet. 36:40-45(2004).

EMBL; AK027753; BAB55344.1; -.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR001110; Ig-1ike.

InterPro; IPR003598; Ig_c2.

Ffam; PR0047; ig_1.

PRANT; SM00408; IGc2; 1.

PROSITE; PS50835; IG_LIKE; 3.
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Sequence 84, Appl Sequence 2, Appli Sequence 2, Appli Sequence 947, App Sequence 615, Ap Sequence 19, Appl Sequence 19, Appl Sequence 1044, A Sequence 10547, A Sequence 6213, Ap Sequence 7850, Ap Sequence 7850, Ap Sequence 7850, Ap Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli

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Searched:

Database

Result No.

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US-09-949-016-11380

i Sequence 11380, Application US/09949016

j Patent No. 681239

j GENERAL INFORMATION:

j APPLICANT: VENTER, J. Craig et al.

i TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

j TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j FILE REFERENCE: CL001307

j CURRENT APPLICATION NUMBER: 60/241,755

pRIOR APPLICATION NUMBER: 60/241,755

pRIOR APPLICATION NUMBER: 60/231,768

pRIOR APPLICATION NUMBER: 60/231,498

pRIOR PLING DATE: 2000-10-03

pRIOR PLING DATE: 2000-09-08

j PRIOR PLING DATE: 2000-09-08

j RIOR SEQ ID NOS: 2077012

j SEQ ID NOS: 2077012

j SEQ ID NO 11380
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US-09-909-064-84
US-09-905-381A-84
US-09-706-618-84
US-09-778-510-2
US-09-205-258-947
US-09-949-016-6515
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US-09-949-016-11043
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US-09-949-016-05313
US-08-485-2
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Matches 167; Conservative
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US-09-984A-1
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                  467
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APPLICANT: Universita degli Studi di Bologna
APPLICANT: Universita Mational de la Sante et de la Recherche M
TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
TITLE OF INVENTION: Medicanent for Preventing or Treating HSV-1, HSV-2 a
TITLE OF INVENTION: BYU Infections
FILE REFERENCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
CURRENT FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 2
128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin
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                                               498 -VENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
                                                              HSV-gD
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31.3%; Pred. No. 1.1e-43;
tive 75; Mismatches 169; Indels
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COTHER INFORMATION: Original Source: Hela Cell Line
OTHER INFORMATION: General Functional Class of Gene:
OTHER INFORMATION: Superfamily
OTHER INFORMATION: Binding Macromolecules: HSV-gD
OTHER INFORMATION: Subcellular localisation: Plasma by
OTHER INFORMATION: Other Information: Viral Receptor US-09-435-956A-1
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                                                                                                                                                      Sequence 1, Application US/09435956A
Patent No. 6469155
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 7563, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PELING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 7563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 NYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFP 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 BYQG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 GEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RTPGPSPLCPGGGKAQLSSASLLGAGLL--LQPPTPPPLLLLLFPLLLFSRL-CGALAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 RPPOSGPRASGRAOSPPGPSMARAALLPSRSPPTP----LLWPLLLLLLETGAQDVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
16.2%; Score 472; DB 4; Length 522;
Best Local Similarity 25.5%; Pred. No. 7.4e-35;
Matches 155; Conservative 79; Mismatches 204; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 ISRREWYV 549
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ORGANISM: Human
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Best Local S:
Matches 148
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                                                                                                                                                                                        APPLICANT: COHEN, Gary H.
APPLICANT: EISEMBERG, Roselyn J.
APPLICANT: EISEMBERG, Roselyn J.
APPLICANT: EISEMBERG, Roselyn J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Clade
APPLICANT: WINVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290.0050/201;
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 1098-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR PLILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 463; DB 4; Length 479;
25.7%; Pred. No. 4.4e-34;
ive 76; Mismatches 184; Indels 168; Gaps
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                                                                                            APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPERK, Patricia G.
APPLICANT: WARNER, MORGYN S.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MARTINEZ, WANDA M.
                                                                                                                                                                             MONTGOMERY, Rebecca I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AG----IFCYRRRTF----
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US-09-94-016-6278

Sequence 6278

Sequence 6278

Sequence 6278

Sequence 628. Application US/09949016

Sequence 628. Application US/09949016

Sequence 628. Application US/0999016

SEGUENCE INVENTION:

APPLICANT: VEWTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PASE SEQ IC Windows Version 4.0

SEQ ID NO 6278
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514 LKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
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TYPE: PRT
ORGANISM: Human
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                                                   APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 HGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAV 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 APEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 PPEVSISGYDNNWYLGQNEATLTCDARSNPEPTGYNWSTTWGPLPPFAVAQGAQL-LIRP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGESGSMAVFHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQY 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKCLJEVNET----ITQISWEKI 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGD
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                                                                                                                                                                                                                                                                                                                                                                                                             83;
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Patent No. 6380362
GRNERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Wurison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for t
                                                                                                                                                                                                                                                                                                                                                                           13.7%; Score 397.5; DB 4; Length 4 26.9%; Pred. No. 4.9e-28; ive 71; Mismatches 183; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                              US-09-949-016-7564
-09-949-016-7564
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Best Local S
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Squence 6729, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-08

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 FKS--VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GSTTLHCSLTSNENVTITQITWMKKDSGGSHALVAVFHPKKGPNIKEPERVKFLAAQQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AQLARAT------RSPLSWLLLLF------CYALRKAGGDIRVLVPYNSTGVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.5%; Score 391; DB 3; Length 408; 28.0%; Pred. No. 1.6e-27; tive 71; Mismatches 178; Indels
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Mouse
US-09-724-864-62
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187 ETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                412 GALFIVLVSVLAGIFCYRRRRTFRGDYFAKN 442
                                                                                                                                                                                                                                                                    379 GVVAVVVFAMLCLLI-----ILGRYFARH 402
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Patent No. 6596493
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 32
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US-09-930-803-1
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                                                                                                                                                       94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                            DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                  DLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
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                                                                                            44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK
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                                                               61;
                                 DB 4; Length 417;
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                               13.4%; Score 390.5; DB 4; 27.6%; Pred. No. 1.9e-27; iive 68; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baum, Peter
TTON: Molecules Designated B7L1
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FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-20-7
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
SPRIOR FILING DATE: 1998-08-07
SOFTWARE: PATENTIN VOIC: 2.0
SOFTWARE: PATENTIN VET: 2.0
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GENERAL INFORMATION:
APPLICANT: Baum, Peter
                               Query Match 13.4
Best Local Similarity 27.6
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapien
   JS-09-949-016-6729
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US-09-778-510-20
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US-09-778-510-20
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APPLICANT: REEVES, ROGER
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHUJ770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 PTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATI------KDDTIATIIASVVG 411
                                                                                                                                                     299 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDP 358
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                                                    GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPP
                                                                                                                                                                                                                                                      PITITLOPTIOWHPSTADIEDLATEPKKLPFPLSTLATI------KDDTIATIIASVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.5%; Score 335.5; DB 4; Best Local Similarity 25.5%; Pred. No. 2.7e-22; Matches 115; Conservative 87; Mismatches 182;
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HILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE SEPERENCE: PEASOR PRIOR PRIOR PELLORATION NUMBER: US/09/944,457

CURRENT APPLICATION NUMBER: US/08/66,028

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: December 13, 1997

PRIOR PILING DATE: December 11, 1997

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APPLICATION NUMBER: PCT/US98/25108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/070,440 FILING DATE: January 5, 1998 APPLICATION NUMBER: 60/074,086
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
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APPLICATION NUMBER: 60/075,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: December 17, 1997
APPLICATION WNWBER: 60/069,873
APPLICATION OFFE December 17, 1997
APPLICATION NUMBER: 60/068,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICATION NUMBER: 60/074,092
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RESULT 14
US-02-944-457-61
Sequence 61, Application US/09944457
Patent No. 6734288
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC:
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
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                                                                                               Sequence 61, Application US/09866028
Patent No. 6642360
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Filvaroff, Ellen
Gerritsen, Mary
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Best Local Similarity 25.7
Matches 117; Conservative
                                                                                                                                                                                         APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Roy, Margaret
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                   Eaton, Dan
                                                                                                                                                            GENERAL INFORMATION:
                                                                           -09-866-028-61
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                                                                                                                  Sequence 22, Application US/09778510 Patent No. 6512095
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Best Local Similarity 26.2
Matches 111; Conservative
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381 FARH 384
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                 US-09-778-510-22
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: Warch 3, 1999
PRIOR FILING DATE: Jane 22, 1999
PRIOR PELING DATE: Jane 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. 6/34286ember 30, 1999
PRIOR FILING DATE: No. 6/34286ember 30, 1999
PRIOR PLICATION NUMBER: PCT/US99/28301
PRIOR PLILING DATE: December 1, 1999
PRIOR PLILING DATE: December 1, 1999
PRIOR PLILING DATE: December 16, 1999
PRIOR PLILING DATE: December 16, 1999
PRIOR PLILING DATE: Pebruary 11, 2000
PRIOR PLILING DATE: Pebruary 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0841
PRIOR PLILING DATE: Pebruary 22, 2000
PRIOR PLILING DATE: Pebruary 22, 2000
PRIOR PLILING DATE: March 2, 2000
PRIOR PLILING DATE: March 30, 2000
PRIOR PLILING DATE: March 30, 2000
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PRIOR PRIOR PLILING DATE: March 30, 2000
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PRIOR PRIOR PLILING DATE: March 30, 2000
PRIOR PRIOR PLILING DATE: March 2, 2000
PRIOR PRIOR PLILING DATE: March 30, 2000
PRIOR PRIOR PLILING DATE: March 30, 2000
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PRIOR PRIOR PLILING DATE: March 30, 2000
PRIOR PRIOR PLILING DATE: March 30, 2000
PRIOR PLILING DATE: March 30, 2000
PRIOR PLILING DATE: PEDRUARY 28, 2001
PRIOR PLILING DATE: PEDRUARY 28, 2001
PRIOR PLILING DATE: PEDRUARY 28, 2001
PRIOR PRIOR PLILING DATE: PEDRUARY 28, 2001
PRIOR PRIOR PLILING DATE: PEDRUARY 28, 2001
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Matches 117; Conservative
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155 LGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGNETVAAICIAATGKPVAHIDW-EGD--- 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 HPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 --PQESYTTITVLVPPRNLMIDIQKDTAVEG--EEIEVNCTAMASKPATTIRWFKGNKEL 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 KLPFPLSTLATI-----KDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 PPPL-LILLEPLILESRICGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 325.5; DB 4; 26.2%; Pred. No. 2.1e-21; tive 79; Mismatches 175;
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
                                                                                                                               PCT/US99/17906
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Job time: 24.9914 secs
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1998-08-07
                                                                                                                     PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR PELICATION NUMBER:
PRIOR PELICATION NUMBER:
PRIOR FILING DATE:
NUMBER:
SOFTWARE:
SOFTWARE:
Patentin Ver: 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
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17;

154

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October 6, 2005, 09:13:38 ; Search time 255.269 Seconds (without alignments) 894.712 Million cell updates/sec
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Sequence 12,
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                                                                                                                                                                                                                                2905
1 MARTPGPSPLCPGGGKAQLS......BDDLVSHVDGSVISRREWYV
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22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1,6
(c) 1993 - 2005 Compugen Ltd.
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US-09-972-268-6
US-010-161-568-5
US-09-972-268-2
US-09-959-845-2
US-09-972-268-17
US-09-972-268-15
US-09-972-268-15
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US-09-972-268-14
US-09-972-268-12
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                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 16, Appl Sequence 8, Appli Sequence 31, Appl	4.1	sequence 6, Appii Sequence 19, Appl Sequence 2626, Ap	Sequence 50, Appl Sequence 20, Appl	Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl	31	33,	99	54,	i m r	6	Sequence 11, Appl Sequence 17, Appl	22	Sequence 30, Appl Sequence 36, Appl	40,	41,	Sequence 42, Appl Sequence 82, Appl	7
US-09-972-268-16 US-09-972-268-8 US-09-972-268-31	US-09-959- US-09-972-	US-09-959-845-6 US-09-972-268-19 US-10-264-237-2626	;	US-US-919-1/2-20 US-10-752-986-20 US-09-972-268-21		US-09-766-511B-33 US-10-241-220-94	US-1	US-1	US-10-422	US-10	US-10-422-571-11 US-10-422-571-17	US-10-422-571	US-10-422-571-30 US-10-422-571-36	US-10-422-	US-10-422-	US-10-422-571-42	US-10-422-571-1
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ALIGNMENTS

US-09-972-268-4

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Sequence 4, Application US/09972268
Publication No. USZ0030044893A1
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Sorensen, Enic A.
APPLICANT: Lofton, Timothy E.
APPLICANT: Journal, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITELE REPERBENCE: 3101-A
CURRENT FILING DATE: 2000-10-05
TITLE REPERBENCE: 300-10-05
CURRENT FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER: OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: S49
TYPE: PRIOR ARTIficial Sequence
FEATURE:
OTHER INFORMATION: mucleotides 1-21 are from Mus musculus Nectin-3, the rest are from CHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4
QUETY MACCh
Best Local Similarity 100.0%; Pred. No. 1.4e-214;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-161-572-45

US-10-161-572-45

US-10-161-572-45

US-10-161-572-45

Publication No. US20030087266A1

GENERAL INFORMATION:

TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-097C-PC

CURRENT APPLICATION NUMBER: US/10/161,572

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 60/296,076

PRIOR APPLICATION NUMBER: US 60/396,056

PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR PILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/338,733

PRIOR PILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/357,253

PRIOR PILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VERSION 3.1

SOFTWARE: PATENTIN VERSION 3.1

SOFTWARE: PATENTIN VERSION 3.1
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                241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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                                                                               TITLOPTIOWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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99.6%; Pred. No. 3.4e-213;
tive 0; Mismatches 2;
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Best Local Similarity 99.6
Matches 547; Conservative
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publication No. US20030044893A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Lofton, Timothy E.
APPLICANT: Soronsen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE YELER REPRENCE: 3101-1-A
CURRENT PAPLICATION NUMBER: US/09/972,268
CURRENT PAPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
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                                                                  248 VKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Keiko SATO
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-16784/LC/00653
CURRENT PELLOATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US/09/09/19/PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2000-065595
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09959845; Publication No. US20030008334A1; GENERAL INFORMATION:
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Publication No. US20030044893A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Sorensen, Timochy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Baun, Polymertides, Polymucieotides, Methods of Making And USE TITLE OF INVENTION: NGCTIN POLYPEPTIDES, POLYMUCIEOTIDES, METHODS OF MAKING AND USE CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: US/09/972,268
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llarity 100.0%; Pred. No. 1.4e-211;
Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
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LENGTH: 542
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Eanslow, William C.
APPLICANT: Canciby E.
APPLICANT: Location, Timethy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 05/238,557
PRIOR APPLICATION OF: 39
SOFTWARE OF SEQ ID NOS: 39
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 15
LENGTH: 426
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US-09-972-268-15
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
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APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sociensen, Eric A.
APPLICANT: Sociensen, Exic A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYNUCLEOTIDES, METHODS OF MAKING AND USE CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 00/238,557
PRIOR PRILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
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Best Local Similarity 93.33
Matches 512; Conservative
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APPLICANT: Baum, Peter R.

APPLICANT: Fanalow, William C.

APPLICANT: Fanalow, William C.

APPLICANT: Sorensen, Enic A.

APPLICANT: Sorensen, Enic A.

APPLICANT: Sorensen, Enic A.

APPLICANT: Youakim, Adel

TITLE OF INVENTION: NUMBER: 02(09)972,268

CURRENT APPLICATION NUMBER: 02(09)972,268

CURRENT FILING DATE: 2001-10-05

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 10
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Best Local Similarity 67.9%; Pred. No. 3.3e-139;
Matches 390; Conservative 33; Mismatches 62;
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GENERAL INFORMATION: APPLICANT: BAUM, Peter R.
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US-09-972-268-14
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                     KSVWSRLDGQWPDGLLASDNTLHFVHPLTPNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FC US-09-972-268-13
                                                              TTTLOPTIQMHPSTADIEDLATEPKKLPPPLSTLATIXDDTIAT 404
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US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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US-09-972-268-10
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Milliam C.
APPLICANT: Fanslow, William C.
APPLICANT: Forton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: BOLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PILLING DATE: 2000-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.6%; Score 1906.5; DB 10; Lengt
Best Local Similarity 67.6%; Pred. No. 8.1e-138;
Matches 388; Conservative 33; Mismatches 64; Indels
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    CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO: 12
LENGTH: 510
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-972-268-12
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APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Soremaen, Eric A.
APPLICANT: Soremaen, Eric A.
APPLICANT: Soremaen, Eric A.
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
SOFTWARE: Patentin version 3.1
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 65.6%; Score 1907; DB 10; Length 595; Best Local Similarity 76.4%; Pred. No. 9.2e-138; Matches 383; Conservative 16; Mismatches 70; Indels 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 PDSVKKENK---NPVNNLIRK 484
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ORGANISM: Artificial Sequence
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US-09-972-268-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 14
LENGTH: 595
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanalow, William C.
APPLICANT: Fanalow, William C.
APPLICANT: Sorensen, Exic A.
APPLICANT: Sorensen, Exic A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE REPERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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                                                                                                                       SINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGN 186
                                                                                                                                                                                                   ETVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITC 246
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                                                                 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNY
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PSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHV
                                          TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNY
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 78.99
Matches 370; Conservative
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| Publication No. US20030044893A1
| GENERAL INFORMATION:
| APPLICANT: Baum, Peter R. |
| APPLICANT: Fanalow, William C. |
| APPLICANT: Forelow, William C. |
| APPLICANT: Sorensen, Exic A. |
| APPLICANT: Sorensen, Exic A. |
| APPLICANT: Sorensen, Med |
| TILLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T. |
| TILLE OF INVENTION: NUMBER: US/09/972,268 |
| CURRENT PELICATION NUMBER: 60/238,557 |
| PRIOR FILING DATE: 2000-10-05 |
| NUMBER OF SEQ ID NOS: 39 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 8
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Pred. No. 3.5e-137;
0; Mismatches 4;
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Best Local Similarity 67.6%; Pred. No. 9.5e-137;
Matches 384; Conservative 33; Mismatches 62;
                                                                                                                                          ; OTHER INFORMATION: fusion protein: US-09-972-268-16
  NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                     Query Match
Best Local Similarity 98.9%;
Matches 359; Conservative (
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Publication No. US20030008334A1
GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Kesiko SATO
APPLICANT: Kenichi TAKAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/JP01/01871
PRIOR APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: JP 2000-065595
PRIOR APPLICATION NUMBER: JP 2000-065595
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
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Best Local Similarity
Matches 376; Conserv
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Search completed: October 6, 2005, 09:33:41 Job time : 257.269 secs Human pol Human pro Human IG

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Human Ig

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Human, nectin-Jalpha, therapy, cell adhesion, cell proliferation, sepsis, paracellular transport disorder, kidney, diabetic retinopathy, allergy, allograft rejection, metastasis, restenosis, inflammatory, bowel disease, oedema, atherosclerosis, ischaemia reperfusion injury, thrombosis, stroke, tumour, cancer, herpesvirus infection, asthma, chromosome 3.
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/note= "Extracellular Ig domain"
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AAY32390
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ADO47877
ADK83174
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ABC05562
ABR48229
ABU56613
ABP97212
ADM42033
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                          gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRRITCVVXHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                       purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation or anglogenic condition of a tissue or a subject, unch as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular sequence is human nectin-Jalpha DNA. Human nectin-Jalpha gene is located on chromosome 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARTIRPSPLCPGGGKAQLSSASILGAGLLLQPPTPPPLLILLFPLILFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                              invention relates to a substantially purified nectin3alpha, beta
                                                                                                                                                                                             useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
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                                                                          Youakim A;
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                                                                            Sorensen EA,
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                                                                                                                                                                                                                                                                        Claim 1; Page 89-91; 141pp; English.
                                                                            Lofton TE,
05-OCT-2000; 2000US-0238557P.
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Matches 549; Conservative
                                                                            Fanslow WC,
                                    (IMMV ) IMMUNEX CORP
                                                                                                                2002-426103/45
                                                                                                                                   N-PSDB; AAD37442.
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The invention relates to a novel method for identifying a candidate p53 pathway modulating agent. The method comprises providing an assay system having a purified IG polypeptide or nucleic acid, or their functionally active fragment or derivative. The method is useful for identifying modulators of the p53 pathway, particularly for identifying agents for treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung cancer or cancer of the ovary) associated with defective p53 function. The identified modulators are useful as taxgets for novel therapeutics. The method is also useful for diagnosing disorders associated with defective p53 function. The IG proteins or nucleic acids are useful as modifiers of the p53 pathway, and as therapeutic targets for disorders associated with defective p53 function. This sequence represents a human protein relating to the human IG genes used in the assay for identifying modulators of the p53 pathway of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate p53 pathway modulators that are useful as targets for therapeutics or for diagnosing cancers associated with defective p53 function, by providing an assay system having a purified IG polypeptide
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                             481 LIRKDYLEEPEKTQWNNVENLNRPERPMDYYEDLKWGMKFVSDEHYDENEDDLVSHVDGS
481 LIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
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100.0%; Pred. No. 2.1e-233;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene related protein SEQ ID No
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                                                                                                                                                                                                                                                                                                           ABJ20222 standard; protein; 549 AA.
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2001US-0328605P.
2001US-0338733P.
2002US-0357253P.
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                                                                                                           VISRREWYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kidney cancer;
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This invention describes novel cytostatic polynuclectide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection of substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, contrainterfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody directed against Ab or any of the above derivatised or thun a reporter group, cell toxin, immunostimulatory molecules and/or (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-buman CD4 murine monoclonal antibodies; between counterstained with hemalum (blue). Malignant cells stained samples were counterstained with hemalum (blue). Malignant cells stained surongly but non-malignant cells only weakly. In 15 of 61 samples of adancearcinoma, membrane and cytoplasmic staining was very strong, and surongly but non-malignant cells only weakly. In 15 of 63 samples of in the method of the
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                                                  New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
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; Pred. No. 2.1e-233;
0; Mismatches 0;
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Local Similarity 100.0%;
es 549; Conservative 0;
                   WPI; 2004-653386/63.
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Rosenthal A, Hermann K, Pilarsky C, Specht T; S, Bruemmendorf T, Kinnemann H, Roepcke S;
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14-MAY-2003; 2003DE-01022134.
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Beckmann G,
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ROSENTHAL A.
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between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CDL4 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; belotinylated second antibody, streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. AbRSS805-ADRS6554 represent the polymucleotide and polypeptide sequences used in the method of the
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100.0%; Pred. No. 2.1e-233;
iive 0; Mismatches 0;
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                                         VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNN
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14-MAY-2003; 2003DE-01022134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, is includential, acheroselerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3 alpha gene is a located on chromosome 3. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse; stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%; Score 2887; DB 5; Length 549; 99.6%; Pred. No. 3.1e-232;
                                                                                                                                                                                                                                                                                                                                                                                                   Lofton TE, Sorensen EA, Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                               "Human nectin-3alpha protein"
                                                                                                                                                                                 "Mouse nectin-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 80-82; 141pp; English.
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                          2001WO-US031392.
                                                                                                                                                                                                                                                                                                                                      05-OCT-2000; 2000US-0238557P.
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/note= "I
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                                                                                                                                                                                                                                                                                                                                                                                                    Baum PR, Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-426103/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 547; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD37441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 549 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sepsis, stroke.
                                                                                                                                                                                                                                             WO200228902-A2
                                                                                                                                                                                                                                                                                                        05-OCT-2001;
                                                               chromosome 3
                                                                                           sapiens
                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                            11-APR-2002
                                                                                                                      Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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Human; nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Youakim A;
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Human deleted nectin-3alpha protein.
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(first entry)

22-OCT-2001

AAM39143;

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The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Sectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above matrioned method is inflammation, sepsis, oedema, diabetic retinopath, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothemial cell, an epithelial cell or a smooth muscle cell). The present sequence is human nectin-3alpha protein containing 7 amino acids deleted from the N-terminal end. Human nectin-3alpha protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AVWCKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLFPTRFARGRRITCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLILLLFPLLLFSRLCGALAGPITVEPHVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.8%; Score 2866; DB 5; Length 542; 100.0%; Pred. No. 1.7e-230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 542 AA;
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540 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFC 427 YRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYL 487 EEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREW 547 EEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREW YV 549 542 -≥ 361 428 421 488 481 368 엄 g ઠે ò g ò

VWGKONVSLKCLIEVNETITQISWEKIHGKSSQIVAVHHPQYGFSVQGEYQGRVLFKNYSL 128

PLCPGGGKAQLSSASLLGAGLLLQPPTPPLLLLFPPLLLFSRLCGALAGPIIVEPHVTA

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AAM39143 standard; protein; 555 AA.

AAM39143 ID AAM3 XX RESULT 7

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encoded polypeptides (AAM88642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-braquer Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, Activin/inhibin activity, chemotactic/chemokinetic activity, Acceptance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                  nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                  peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; hemostatic; amyotrophic lateral sclercosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2856; DB 4; Length 555;
Pred. No. 1.2e-229;
0; Mismatches 1; Indels (
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Yang Y,
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ΑJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ma Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen R,
Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodrich R, Drmanac RT;
                                                             Human polypeptide SEQ ID NO 2288.
                                                                                                                                                                                                                                                                                                                                                              23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUL-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match
Local Similarity 99.8%;
nes 540; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Asundi V,
Wang Z, Wehrman T,
                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                           leukaemia.
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Wang J,
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240 300 300 360 360 420

120 120

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and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynuclectides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                    IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                              VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                                                                                                                                           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTLQPT1QWHPSTAD1EDLATEPKKLPFPLSTLAT1KDDT1AT11ASVVGGALF1VLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer.
                                                                                                                                    1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell infiltration; cancer metastasis;
                                                                                                              Indels
                                                                                          Length
                                                                                                              20;
                                                                                       Score 2721; DB 4;
Pred. No. 2.4e-218;
19; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of murine nectin-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549
                                                                                        93.8%;
92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                   Best_Local Similarity 92.99
Matches 510; Conservative
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                                                                   Sequence 549 AA;
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                                                                                                                            KHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLD 314
                                                                                                                                                                       G@WPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTLQPTI 374
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 VWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL
                                   VAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVV
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                                                                                                             KHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLD
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AAE23291 standard; protein; 549

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                                                                      Nakanishi H,
                           JAPAN SCI & TECHNOLOGY CORP
TAKAHASHI K.
09-MAR-2000; 2000JP-00065595
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Matches 510; Conservative
                                                                                                                                                                          corresponding antibodies.
                                                                      Takai Y,
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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymuclectides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial adhesion activity, viral polypeptide binding activity. The epithelial or migration activity, viral polypeptide binding activity. The above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, astenday, allersy, allograft resjection, meteateably the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, parcellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenesis, ischaemia-reparfuss or a subject, such as ischaemia, atherosalerosis, ischaemia-reparfushon injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (Vascular sequence is mouse nectin-3alpha protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                         Mouse; nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metrastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR
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                                                                                                                       Mouse nectin-3alpha protein.
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RESULT 10 AAE23291

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic acitvity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosasis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, hemostatic and thrombolypitic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLD 308
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              such
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            disorders
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            treating
                                                                                                                                                                                                                                                                                                                                                          33; Indels
            for
                                                                                                                                                                                                                                                                                                                              Query Match

88.5%; Score 2568.5; DB 4;
Best Local Similarity 91.3%; Pred. No. 1.4e-205;
Matches 504; Conservative 4; Mismatches 33;
           nucleic acids and polypeptides, useful
                                                  Example 2; SEQ ID NO 5860; 10078pp; English
                        central nervous system injuries
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, Zhao Q
                                                                              GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; hamenstatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
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Yang Y,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00598042.
19-JUL-2000; 2000US-006531450.
14-SEP-2000; 2000US-00653191.
19-CCT-2000; 2000US-00653191.
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1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI

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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymuclecides. Mectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding polymuclecides. Corresponding polymuclecides.

To endothelial barrier function activity, endothelial proliferation or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, astacellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

To endothelial cell, an epithelial cell or a smooth muscle cell (vascular procedulation or migration of an endothelial cell). The present sequence is human nectin-3alpha-
                                                                                                      Human; nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
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    .404
/note= "Human nectin-3alpha protein"

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                                                                    nectin-3alpha-FLAGpolyHis fusion protein.
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                                                                                                                                                                                                                                                                                                                                                               /note= "FLAG peptide"
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/note= "PolyHis tag"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200228902-A2
                                                                                                                                                                                                                   Homo sapiens.
Unidentified.
                                   27-AUG-2002
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360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial
                                                                                  121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                            61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                              VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                             LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                             GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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Score 2120; DB 5; Pred. No. 2.9e-168; 0; Mismatches 2;

73.1%; 99.5%;

Conservative

402;

Similarity

Local

Best Loca Matches

Query Match

Length 426;

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migration activity, viral polypeptide binding activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paraecallular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing human nectin-Jalpha protein fused to immunoglobulin IgGl Fc region
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                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                              73.1%; Score 2120; DB 5; 99.5%; Pred. No. 5.3e-168; ive 0; Mismatches 2;
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Matches 402; Conservative
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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens juuction formation activity, epithelial corresponding barrier function activity, endothelial proliferation or majoration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastashs of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, condition of a tissue or a subject, such as stroke, restenosis, immour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an endothelial cell), an epithelial cell or a smooth muscle cell (vascular martin-late and man and man nectin-labeta protein.
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/note= "Intracellular C-terminal domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%; Score 1920.5; DB 5; 67.9%; Pred. No. 1.8e-151; ive 33; Mismatches 62;
                                                                                                                                 /note= "Extracellular Ig domain"
222
'note= "Extracellular Ig domain"
                                                                                                                                                                                                                 /note= "Extracellular Ig
                                    note= "N-glycosylated"
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186
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                                                                                                      /note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2001; 2001WO-US031392
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Best Local Similarity 67.9%
Matches 390; Conservative
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The invention relates to a substantially purified nectinialpha, beta, comma and nectin-4 polypeptides and their corresponding polynucleotides. CC gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with call adhesion activity, adherens juuction formation activity, epithelial cc or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or condition disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenic condition of a tissue or a subject, such as isolaemia, atherosclerosis, isohaemia-reperfusion injury, thrombosis, isohaemia, atherosclerosis, isohaemia-reperfusion injury, thrombosis, stroke, restenosis, immour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a semooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein encoding 6 amino acids from mouse nectin-3 protein and the rest form human nectin-3 beta agene is located on chromosome 3.

CC (Updated on 29-AUG-2003 to standardise OS field)
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Best Local Similarity 67.6%; Pred. No. 2.7e-150;
Matches 388; Conservative 33; Mismatches 64;
                                                                                                                                                                                                  Claim 1; Page 94-95; 141pp; English
2002-426103/45.
                       N-PSDB; AAD37444
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                                                                                                                                                   sepsis, stroke.
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Search completed: October 6, 2005, 09:51:32 Job time : 92.6763 secs

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GenCore veraion 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	. October 6, 2005, 09:42:42 ; Search time 18.0493 Seconds (without alignments) 2926.593 Million cell updates/sec
	OM protein -	Run on:

US-09-972-268-6 2901 1 MARTLRPSPLCPGGGKAQLS......BDDLVSHVDGSVISRREWYV 549 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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:	Description	hypothetical prote	poliovirus recepto	poliovirus recepto		PRR2 alpha - human		poliovirus recepto	poliovirus recepto	poliovirus recepto	poliovirus recepto	colon carcinoma-as	irregular chiasm C	perlecan precursor	hypothetical prote	hemicentin precurs	adhesion molecule	surface glycoprote	neural cell adhesi	OX-2 membrane glyc	elastic titin - hu	heparan sulfate pr	DM-GRASP precursor	Down syndrome cell		adpe	neural cell adhesi	myelin-associated	SHP substrate-1 pr	fibroblast growth
SUMMARIES	ID	T08732	JC4024	HLMSP3	A53437	153960	I68093	A44194	B44194	RWHUPD	RWHUPA	A54017	A49448	A38096	T20992	T43290	JH0506	A45254	IJBONC	A47639	I38346	S18252	JH0464	T08851	JH0371	IJRTNC	IJHUNG	B33785	JC5289	B49151
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ALIGNMENTS

RESULT 1 T08732 Mypothetical protein DKFZp566B0846.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: T08732 C;Accession: T08732 C;Accession: T08732 A;Rottenwaelder, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16474 A;Accession: T08732 A;Accession: T08732 A;Accession: T08732 A;Accession: T08732 A;Accession: T08732 A;Accession: T0874 A;Accession: T0874 A;Accession: T0876 A;Accession: T	Query Match Best Local Similarity 99.3%; Pred. No. 6.1e-146; Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	143 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAALCIAATGKPVA 202 	203 HIDWEGDLGEMESTTTSFPNETATIISQYKLFFTRFARGRRITCVVKHPALEKDIRYSFI 262 	263 LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL 322 	323 HFVHPLTENYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT 382 	383 EPKKLFFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDYFAKN 442 	443 YIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYLEEPEKTQMNNVENLN 502 	503 RFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 549
RESULT 1 T08732 hypothetical pi C;Species: Hounc C;Date: 11-Jun. C;Accession: TG R;Ottenwaelder, Submitted to ti A;Reference nur A;Recession: TG A;Molecule type A;Residues: 1-4 A;Residues: 1-4 A;Residues: C;Genetics: A;Note: DKFZp56	Query Ma Best Loo Matches	& 8	රු සි	රු දු	ò q	රු දි	& 2	දු දු

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poliovirus receptor-related protein precursor - human C.Species: Homo sapiens (man)
C.Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C.Accession: JC4024
C.Accession: JC4024
C.A.C. E. Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr Gane 155, 261-265, 1995
A,Title: Complementary DNA characterization and chromosomal localization of a human gene A,Reference number: JC4024
A,Accession: JC4024
A,Residues: 1-518 <LOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poliovirus receptor homolog precursor - mouse
C,Species: Mus musculus domesticus (western European house mouse)
C,Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C,Accession: A38211
E,Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A,Title: Molecular cloning and expression of a murine homolog of the human poliovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 FIDGTIRLSRLELEDEGVYICEFATFPTGNRESQLNLTVMAXPT-NWIEGTQAVLRAKKG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 YISDPPITITLQPIIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFIVLVSVLAGIF--CYRRRRTFRGDYFAKNYI------PPSDMQKESQIDV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 ILLVLI-VVGGIVVALRRRRHTFKGDÝSTKKHVYGNGYSKAGIPOHHPP--MAQNLQ--- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDDKVLVATCTSANGKPPSVVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVI 353
                                                                                                                                                                                                                                                                                                                                              A/Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C;Genetics: GDB:PVRR1
A;Gene: GDB:PVRR1
A;Gene: GDB:PVRR1
A;Gene: GDB:PVRR1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
C;F2700main: signal sequence #status predicted <AMT>F;1-30/Domain: signal sequence #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain: transmembrane #status predicted <AMT>F;356-379/Domain <AMT>F;35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GNETVAAICIAATGKPVAHIDWE-------GDLGEMESTTTSFPNETATIISQYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 FPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VENLINRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%; Score 627; DB 2; Length 518;
30.8%; Pred. No. 3.7e-37;
.ive 80; Mismatches 177; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOQDELDSYPDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN------
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Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipace: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipacession: A53437
RiAoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with polikeference number: A53437; MUID:94179228; PMID:8112569
                                                                PIDN: AAA39734.1; PID: 9199786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RRRRIF------RGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FGNGG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 VEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPOSV-----AVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DVGPLVWGAVGGTLLVLL---LAGFLALIL 373
                                                                                                                                                                                                                                                                                                                                    F;355-374/Domain: transmembrane #status predicted <TMV>
F;375-467/Domain: intracellular #status predicted <IMV>
F;57-4131,174-229,274-320/Disulfide bonds: #status predicted
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 LLOPPTPPPLLLLEPPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vippsrispripliplililiosrgaqovrvrvipevrgriggtvelpchilpptrervs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASAVAQGSQL-LVHSVDRMVNTTFICTATNAVGTGRAEQVILVRDTPQASR-----
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69; Mismatches 201; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch
al Similarity 27.4%; Pred. No. 1.1e-27;
153; Conservative 69; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 LRGRRRKSPGGGGNDGDRGSYDPKTQV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVFWRSASPEPMRPDGREEDEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467
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DDMESHLDGSLISRRAVYV
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C;Accession: 168093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRRZ gene, related to the human poliovirus receptor gene (PVR), is the A;Reference number: 153960; MUID:95347610; PMID:7622062
                                                                                                       20;
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                                                                                                                                                                                                                                                                                            | : | | | | : | | | : | | : | : | : | HGLTVEDEGNYTCSPATFPKGSVRGMTWLRVIAKPKNQAEAQKYTFSQDP-----T 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | | | | :: | :: | | | 374
                                                                                                                                                                                                                                                         ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF------KNYSLNDATITL 135
                                                                                                                                                                                                                                                                                                                                                              HNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNET 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RGDYFAKNYIPPSDMQKES 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 QIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYED 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGSLAFILLRVRRRKSPGGAGGGASGDGGFYDPKAQVLGNGDPVFWTPVVPGPME--- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                       13 PPTP----LLWPLILLLLERGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                    33 PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
                                                                                                       Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 135;
                                                          Length 478;
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                                                     Query Match
16.0%; Score 463.5; DB 2;
Best Local Similarity 25.5%; Pred. No. 1.8e-25;
Matches 147; Conservative 76; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 LKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KDEBEBEE
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llarity 24.6%; Pred, No. 2.1e-24;
Conservative 91; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
     F;276-331/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
Matches 139; Conserv
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A; Residues: 1-538 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRR2 delta - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: PRR2delta
                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                 128
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A,Accession: A53437
A,Status: preliminary
A,Fistus: preliminary
A,Fistus: preliminary
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: 1530 cAOK>
A,Fistus: Sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C,Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                급
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 PSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAG---IFCY 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 RRRRIFR------GDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNP 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQRKEQRLQAADEEEELEG---PPSYKPPTPKAK-----LEEPEMPSQLFTLGASEHSP 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 VNNLIRKDYLE------DYYEDL 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVTWORLDG---TVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGLR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STGGRPPARITWISSIGG-EAKDIQEPGIQAGIVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWH 371
                                                                                                                                                                                                                                                                                                                                                                                            6 VLPPSRLSPTLPLLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS 65
                                                                                                                                                                                                                                                                                                                                                              30 LLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Dates: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Eberle: F; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene
A;Reference number: 153960, MUID:95347610; PMID:7622062
                                                                                                                                                                                                                                                                                                              Gaps
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C;Genetics:
                                                                                                                                                                                                                                                         Query Match
16.2%; Score 470; DB 2; Length 530;
Best Local Similarity 24.8%; Pred. No. 7.1e-26;
Matches 140; Conservative 90; Mismatches 212; Indels 122;
                                                                                                                                                                                                                                                       Length 530;
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C;Superfamily: poliovirus receptor; immunoglobulin homology
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PRR2 alpha - human
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Qy 206 WEGDLGEWESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRVSFIL 263 179 WHSDLGGWENTSQAPGFLSGTVTVTSLMILVPSSQVDGKSVTCKVEHESFERFQLLTVNL 238 Qy 264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLH 323 1	RESULT 8 B44194 poliovirus receptor (clone AGM-delta-1) - green monkey C;Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 R;Koike, S; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A. Jyithle: A second gene for the African green monkey poliovirus receptor that has no putat A;Reference number: A4194 A;Reference number: A4194 A;Reference number: DNA A;Residues: 1-392 <koi>A;Residues: 1-392 <koi>A;Residues: UNIRROT: P32506; GB:S48817 C;Superfamily: poliovirus receptor; immunoglobulin homology F;259-314/Domain: immunoglobulin homology <mm>></mm></koi></koi>	Ouery Match Best Local Similarity 28.1%; Score 415.5; DB 2; Length 392; Best Local Similarity 28.1%; Pred. No. 3.8e-22; Matches 121; Conservative 72; Mismatches 174; Indels 63; Gaps 16; Oy 37 PPLLILLFPLILESRICGALAGPIUVB-PHYDAWGRAVSLKCIEVNET-ITOIS 90 10 PPLLILLLFSRICGALAGPIUVBPHYDAWGRAVSLKCIEVNET-ITOIS 90 110 PPLLILLLELSWPPFGGDIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT 65 QY 91 WEXHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKYNYSLNDATITLHNIGFSDSGKXI 147 E
Db 13 PPTPLLWPLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL 67 Qy 89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQGRVLFKWYSLNDATITL 135		RESULT 7 A44194 Poliovirus receptor (clone AGM-alpha-1) - green monkey C;Species: Cercoptthecus acthiops (green monkey, grivet) C;Date: 30-Sep-1933 #text_change 09-Jul-2004 C;Date: 30-Sep-1933 #text_change 09-Jul-2004 C;Date: 30-Sep-1933 #text_change 09-Jul-2004 C;Date: 30-Sep-1933 #text_change 09-Jul-2004 R;Koike, S.; Ise, I: Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A. J. Virol. 66, 7059-7066, 1992 J. Matches Ditortur receptor; immunoglobulin homology J. Matches Ditortur receptor; immunoglobulin homology J. Matches Ditortur receptor; immunoglobulin homology J. Matches Ditortur receptor; immunoglobulin homology J. J. PPLLLIEPPLLIESRICGALAGPIIVE-PHYTAVANGRNYSIRCLIEVNET-TTQIS QY J. MEKIHGKSSQTVAVHHPQYGFSVQEYQEYQEYQEYGENEPVARICHARPORNYERPYALIFYANGRNYBETHYRIP 205 J. J. J. J. J. J. J. J. J. J. J. J. J. J

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: $12048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Taker R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Taker R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Taker A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted A;Reference number: $12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-66, A',68-417 <MEN>
A;Cross-references: GB:M29535
C;Coment: The normal function of this receptor is unknown. Membrane-bound and soluble f
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A; Map position: 19413.2-19413.2

A; Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3

C; Superfamily: poliovirus receptor; immunoglobulin homology

C; Superfamily: poliovirus receptor; immunoglobulin homology

C; Reywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro-
F; 1-20/Domain: signal sequence #status predicted csize predicted csize
F; 21-343/Domain: extracellular #status predicted csize
F; 21-343/Domain: immunoglobulin homology csize
F; 259-314/Domain: immunoglobulin homology csize
F; 259-3
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F;368-417/Domain: intracellular #status predicted <INT>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA454
A;Note: 67-Ala was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Noce: the gamma form has 3:1-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, B.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Callular receptor for poliovirus: molecular cloning, nucleotide sequence, and A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 FPLILFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                      387 LPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 390.5; DB 1; 27.6%; Pred. No. 2.6e-20; tive 68; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                            poliovirus receptor splice form alpha precursor - NAlternate names: poliovirus receptor H20A N;Contains: poliovirus receptor beta
301 PVDKPINTTLICNVTNALGARQAELTVQVKEGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GDB:120324; OMIM:173850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 27.6%
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-417 < KOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: PVR; PVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S12048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                        RWHUPD

POPLIONIUS receptor splice form delta precursor - human

NyAlternate names: poliovirus receptor H20B

C;Species: Home sapiens (man)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: A43024; B31496

R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

EMBO J. 9, 3217-3224, 1990

A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted

A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A General GDB: PVR; PVS
A; Gross-references: GDB:120324; OMIN:173850
A; Gross-references: GDB:120324; OMIN:173850
A; Gross-references: GDB:120324; OMIN:173850
A; Cross-references: GDB:120324; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2; 281/2;
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F.368-392/Domain: intracellular #status predicted <INT>
F.49-123,166-221,266-312/Disulfide bonds: #status predicted
F.49-123,166-221,266-312/Disulfide bonds: #status predicted
F.105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Comment: The normal function of this receptor is unknown. Membrane-bound and soluble C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular cloning, nucleotide sequence, and PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLGEMESTT -- TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HGESGSMAVFHQTQQPSYSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIPPOGSRSVDIWLRVILAKPONTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Lype: DNA
A; Residues: 1-392 < KOI.>
A; Cross-references: UNIPROT: P15151; EMBL: X64116
A; Notes: 67-Ala was also found
R; Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A; Title: Cellular receptor for poliovirus: molec
A; Reference number: A90910; MUID: 89168426; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...
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A;Residues: 1-66,'A',68-392 <MEN>
A;Cross-references: GB:M24406
380 LSPSSEHHQS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B31496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
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Qy Db Qy Qy Qy Qy Qy Db Db Colon Calon Oy 267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFRSVWSRLDGQWPDGLLASDNTLHFVH 326	RESULT 12 A4948 irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster) NiAlternate names: irreC-roughest protein C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004 C;Date: 11-Nov-1994 #squence_revision 11-Nov-1994 #text_change 09-Jul-2004 C;Date: 11-Nov-1994 #squence_revision 11-Nov-1994 #text_change 09-Jul-2004 C;Accession: A4948# S34129 R;Ramos, RC Dr. igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandstigenes Dr. 7, 2533-2547, 1993 A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal project A;Reference number: A49448; MUID:94102535; PMID:7503814 A;Status: preliminary A;Residues: 1-764 <ram>A;Residues: 1-764 <ram>A;Cross-references: UNIPROT:Q08180; GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NII C;Genetics: A;Genetics: A</ram></ram>	
A, Katum A, Molecu A, Crossid A, Crossid Int. J. A, Tit. Lo. A, Refert A, Molecu A, Resid A, Note: C, Commer C, Keywor	A,Status: preliminary A,Molecule type: mRNA A,Status: preliminary A,Molecule type: mRNA A,Residues: 1-416 cCIMPROT:Q7M048; GB:L12025 A,Residues: 1-416 cCIMPROT:Q7M048; GB:L12025 B,Cross-references: UNIPROT:Q7M048; GB:L12025 R;Chadencau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K. Int. J. Cancer 47, 903-908, 1991 A,7title: Characterization, isolation and amino terminal sequencing of a rat colon carcin A,Reference number: A61206; MUID:91184910; PMID:2010233 A,Accession: A61206 A,Molecule type: protein A,Residues: 34-41, X', 43-53 cCH2> A,Molecule type: protein A,Residues: 34-41, X', 43-53 cCH2> C,Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cell C,Comment: This 66K protein; membrane protein	Qy 40 LLILEPPLILESRICGAL-AGPIIVEPH-VTAVWGKNVSLKCLIEVNETITQ1 89
Query Best I Matche Qy Db Oy Oy Oy	Query Match 11.4%; Score 331.5; DB 2; Length 416; Best Local Similarity 28.1%; Pred. No. 4.4e-16; 39; Gaps 12; Matches 104; Conservative 56; Mismatches 171; Indels 39; Gaps 12; 8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLFPLLLFSRLCGALAGPITVEPHVT 67 1	255 KDIRYSFI-LDIGYAPEVSVTGYDGNWFVGRKG
8 8 8 8 8 8	IDGGNETVAAI MPQDVAK FARGRRITCVA MARTSPAGWN MARTSPAGWSRLI	396 FSVSNETAGKXYCKANVPGYAELSADAXVYLKASPALGSQKTQYGDVGDTAKIEGFASSSV 385 KKTI 15
qa ,	339 EASEILPPKT 348	RESULT 13 A38096 perlecan precursor - human

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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 22.8%
Matches 103; Conservative
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submitted to the EMBL Data
AiReference number: Z19929
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N; Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote C; Species: Homo sapiens (man)
C; Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 12-Jul-2004
C; Accession: A38096; S19256; $\overline{S}_{1}$7946; A41059; A40306; B33525; A33625; A41736
R; Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Jozzo, R.V.
J. Biol. Chem. 267, 8544-8577, 1992
A; Title: Primary structure of the human heparan sulfate proteoglycan from basement membr tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A; Accession: A38096
A; Molecule type: mRNA
A; Accession: A38096; MUD:92235084; PMID:1569102
A; Molecule type: mRNA
A; Residues: 1-4391 "MURPOT:P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
B; Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
A; Title: Muman basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein adhesion molecules, and epidermal growth factor.
A; Accession: S19256
A; Molecule type: mRNA
A; Residues: 1-57, D', 59-434, A', 436, PL', 438-449, Q', 451-502, A', 503-792, K', 794-908, R', 71-2919, H', 2981-2994, G', 2996-3167, T', 3169-3240, R', 3242-3426, R', 3428-3631, Q', 3633-346, A', Baference : BMBL: K62515
B; Tryggvason, K.
Submitted to the BMBL Data Library, October 1991
A, Reference mimber: RATAGA
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C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembra

C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembra

F; 1-21/Domain: signal sequence #status predicted <81G>

F; 22-4391/Product: perlecan #status predicted <MAT>

F; 22-193/Domain: II <DOM1>

F; 194-530/Domain: II ceceptor ligand-binding repeat homology <LDL1>

F; 285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F; 325-359/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F; 366-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F; 531-1676/Domain: LDL receptor ligand-binding repeat homology <LDL4>
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A;Accession: 877946
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A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425
R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 109, 3199-3211, 1989
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A; Residues: 'RT', 892-908, 'R', 910-1101, 'L', 1103-1132, 'L', 1134-1221, 'L', 1223-1397 < KA2>
A; Cross-references: GB:S76436; NID:9243370; PIDN:AAB21121.1; PID:9243371
R; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo,
Genomics 10, 673-680, 1991
A; Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellul,
A; Reference number: A40306; MUID:91365376; PMID:1679749
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A;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HB3>
A;Note: peptide potentially matches four different regions
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A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
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A,Cross-references: GDB:126372; OMIM:142461
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F,4149-4151/Region: motor neuron attachment (L-R-E) motif
F,429-4101/Region: motor neuron attachment (L-R-E) motif
F,4299-4301/Region: motor neuron attachment (L-R-E) motif
F,55/17/F6/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F,89,554,1755,2121,3072,3105,3279,3780,3835,4068/Binding site: carbohydrate (Asn) (coval
F,2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3018 RLRSPVIS-IDPPSSTVQQGQD-ASFKCLIHDGAAPISLEWKTRNQELEDNVHISPN--G 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||: : || : || 3074 SIIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLSVHGPPTVSVLPEGPVWVKVG 3127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3128 KAVTLEC-VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVC 3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3186 LAQNALGTAQKQVEVIVDTGAMAPGAPOVQAEEAELTVEAGHTATLRCSATGSPAPTIHW 3245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GPIIVE---PHVTAVWGKNVSLKCLIEVNETITOISWEKIHGKSSOTVAVHHPOYGFSVO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T20992; T24733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2925 QPIYIEASSSHVTB--GQTLDLNCVVP-GQAHAQVTWYKRGG----SLPARHQTHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 -LVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGVNLKCNADANPPPFKSVWSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 KVTNSLGQRSDQKVIYIS-----PTIQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARTLRPSPLCPGGGKAQLS-SASLLGAGLL--LOPPTPPPLLLLLFPLLLFSRLCGALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 4391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLRLNQVSPADSGEYSCQVTGSSGTLEASVLVTIEPSSPGPI----
7.5%; Score 216.5; DB 2; 22.8%; Pred. No. 2.2e-06; ative 65; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F15G9.4a - Caenorhabditis elegans
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submitted to the EMBL Data Library, December 1994
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A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL;Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FI5G9.4b
A;Cross-references: EMBL;Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FI5G9.4b
A;Cross-references: G:Genetics: A;Genetics: A;Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .004 AVVNSTHDVLDGEGFALPCVVSGTPPPI-ITW-YLDGR-PITPNSRDFTVTADNTL-IVR 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 PLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT---- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYIÇKAVTFPLGNAQSSTT--VTVLVEPTVSL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NLLITDAQI-----EDQGQFTCIARN-TYGQQSQSTTLMVTGLVSPVLGH 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  892 VPPEEQLIEGODLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PTRFARGR---RITCVVKHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FVGRKGVNLKCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          793 PIIIESPHTVRVNIERQVTLQCL-AVGIPPPEIEWQK---GNVLLATLNNPRYTQLADG-
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%; Score 201; DB 2; Length 5198; Best Local Similarity 25.4%; Pred. No. 3.6e-05; Matches 100; Conservative 50; Mismatches 156; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| : : | | | 1115 VYGDPKPVITWLLDDKPF---TEGVVNEDGSLTI 1145
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            A; Molecule type: DNA
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A; Molecule type: DNA
A; Residues: 1-5175 <WI2>
A; Crose-references: EMBL: Z47070; PIDN: CAA87344.1; GSPDB: GN00028; CESP: F15G9.4a
A; Experimental source: clone T09B9
C; Genetics:
A; Gene: CESP: F15G9.4a
A; Map position: X
A; Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2911/1; 2967/3; 2991/3; 11; 2677/3; 2677/1; 4408/1; 4456/1; 4458/1; 4647/3; 4838/1; 4879/1; 4941/1; 5071/1; 5077/1
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A,Molecule type: mRNA
A,Residues: 1-5198 «VOG>
A,Residues: 1-5198 «VOG>
A,Residues: 1-5198 «VOG>
A,Residues: 1-5198 «VOG>
B,R.Sulston, J.
Submitted to the EMBL Data Library, December 1994
A,Reference number: Z19355
A,Reference number: Z19355
A,Recession: T2093
A,Residues: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-5198 «MIL>
A,Residues: 1-5198 «MIL>
A,Residues: 1-5198 «MIL>
A,Residues: Cenore EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A,Experimental source: clone F15G9
B,References: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A,Experimental source: clone F15G9
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C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43290; T20933; T24734
R;Vogel, B.E.; Hedgecock, E.M.
R;Vogel, B.E.; Hedgecock, E.M.
R;Vogel, Coulombe EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhes
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                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 201; DB 2; Length 5175; 25.4%; Pred. No. 3.6e-05; arive 50; Mismatches 156; Indels 88
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A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 25.43
Matches 100; Conservative
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A;Accession: T43290
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88; Gaps

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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610301B19 product:poliovirus receptor-related
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                 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279553; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency_full-length_cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
Tachibana K., Mizoguchi A., Takahashi K., Miyahara M.,
"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                                                                       VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNN
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   TTTLQPT1QWHPSTAD1EDLATEPKKLPFPLSTLAT1KDDT1AT11ASVVGGALF1VLVS
                                                                                                                                      LIRKDYLEEPEKTOMNNVENLNRFERPMDYYEDLKWGMKFVSDEHYDENEDDLVSHVDGS
                                                                                                                                                       LIRKOYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
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                                                                     VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00010, IG; 1.
PS50835; IG_LIKE; 3.
F.10 AA: 60582 MW; 5492C9ABB472F185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U. Biol. Chem. 275:10291-10299 (2000).

EMBL; AF195833; AAF63685.1; -.

MGD; MG1:1930171; Pvr13.

GO; GO:0005913; C:cell-cell adherens junction; IDA.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0005615; F:extracellular space; TAS.

GO; GO:0005615; F:procean binding; IPI.

GO; GO:0016337; P:cell-cell adhesion; IDA.

InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Pred. No. 2.2e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion molecule nectin-3 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 92.9
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                     VISRREWYV 549
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SMART; SM0040
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Pvrl3
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181 HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT
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                                                                                                                               LIRKDYLEBPEKTOWNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI
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  TTTLQPTVQWHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGGALFLVLVS
                                         VLAGI FCYRRRRTFRGDYFAKNY I PPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.8%; Score 2141; DB 2; Length 407; 99.3%; Pred. No. 2.9e-151; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Kidney;
Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL050711; CAB43256.1;
PIR; T08732; T08732.
InterPro; IPR007110; Ig-11ke.
PROSITE; PS50835; IG_LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein DKFZp566B0846 (Fragment).
Home=DKFZp566B0846;
Home sapiens (Human).
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Matches 404; Conservative
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                                                                                                                                                                                                                                                                 541 VISRREWYV 549
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SEQUENCE
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ID Q9Y412
AC Q9Y412;
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SEQUENCE FROM N.A.

Adachi J., Alzawa K., Akhahira S., Akimura T., Arai A., Aono H.,
Adachi J., Alzawa K., Akhahira S., Fukunishi Y., Furuno M.,
Adachi J., Alzawa K., Akhahira S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,
A Macuyama T., Miyazaki M., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Kawai J., Kojima Y., Cono H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Cono H., Kouda M., Koya S., Kurihara C.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shiragawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Antamatau M., Hayashizaki Y.;
RUDI MCDI M., Hayashizaki Y.;
RUDI MCDI MCDI C. Cell-Cell adherens junction; IDA.
GO; GO:0005913; C.cell-cell adherens junction; IDA.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016317; P:protein binding; IPI.
DR InterPro; IPR007110; Ig-like.
BRINEPRO; IPR00710; Ig-like.
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             STRAIN-CSTBL/61; TISSUE-Whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Hateunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsuninoto H., Sakaguchi S., Ikegami T., Kashikwagi K.,
Fujiwake S., Inoue K., Togawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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91.4%; Pred. No. 4.3e-191;
ive 22; Mismatches 25;
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SMART; SM00409; IG; 1.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Haith F.,

Districtenko, L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rayakanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strauberg R., Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases. Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC067808; AAH67808.1; -. InterPro; IPR0031599; Ig. InterPro; IPR0031599; Ig. InterPro; IPR000110; Ig-like. Pfam; PF00047; ig; 1. SMART; SM00409; IG; 1. PROSITE; PS50835; IG LIKE; 3. SEQUENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64;
                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                     Last sequence update)
                             366 AA
                                                       Created)
                                                      27,
27,
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
                             PRELIMINARY;
                                                                                05-JUL-2004 (TrEMBLrel.
                                                                     (TrEMBLrel.
                                                      (TrEMBLrel.
                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=9606;
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                                                       05-JUL-2004
                                                                     05-JUL-2004
                                                                                                           Name=PVRL3;
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RESULT 5
Q6NVZ3
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241 GRRITCVVKHQALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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                                                                                                                     301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYIS 356
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SWART; SM00409; IG; 1.
PROSITE; PS50835; IG LIEE; 3.
SEQUENCE 510 AA, 55811 MW; 45CFBGEF78454864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:10291-10299 (2000).

EMBL; AF155834; AAF63686.1; -.
MGD; MGI:1930171; Pvr13.

GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:integral to membrane; TAS.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0016337; P:cell-cell adhesion; IDA.
InterPro; IPR003599; IG.
InterPro; IPR007110; I9-11ke.
                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                 510 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion molecule nectin-3 beta
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                      301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQKVIYISDIPL
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  GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                               KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT
                                                                                                                                      TTTLOPTIOWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 CVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTLQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                       384 VFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPVYEERIPSLPOKDL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lumitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL/Secondary AAH01305.1; -- InterPro; IPR07110; Ig-like. PROSITE; PSS0815; Ig-like; I. NON TER 1. SEQÜENCE 304 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Similar to nectin 3; DKFZP566B0846 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%; Score 1629; DB 2; L
100.0%; Pred. No. 3.2e-113;
ive 0; Mismatches 0;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 AA
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Best Local Similarity 100.0
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                            VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQQDEL----DSYPDSVKK 472
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  ---SSIA------VAGAVIGAVLALFIIT 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291; Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M., Tachibana K., Mizoguchi A., Takaki Y.; "Tachibana K., Mizoguchi A., Takaki Y.; "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                                                           : | : : | | : : : | | 442 KEKGAGGLQPSNGPISRRFDYEDESTMQEDGTQRMCPLYSQMCHQDRSPR-----QHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENK-----NPVNNLIRKDYLEEPEKT-QWNNVENLNRFERPMDYYEDLKMGMKFVSDEHY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.4%; Score 1809.5; DB 2; Length 76.2%; Pred. No. 1.8e-126; ive 25; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SHUWAYS, T., -. PROSITE; PS50835; IG_LIKE; 3. PS50835; IG_LIKE; AP261 MW; ZAOA4416E5B02FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1930171; PvrI3.
GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005515; F:protein binding; IPI.
GO: GO:0016337; P:cell-cell adhesion; IDA.
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Name=Pvrl3;
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J. Biol. Chem. 275:10291-10299(2000)
EMBL; AF195835; AAF63687.1; -.
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GO; GO: 0005615; C:extracellular
GO; GO: 00016021; C:integral to m
GO; GO: 0005515; P:protein bindi
GO; GO: 0016337; P:cell-cell adh
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
Pfan; PF00047; 1g; 1.
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Best Local Similarity
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MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
Leccoq E., Dubreuil P., Campadelli-Filume G.;
"The murine homolog of human nectin1 delta serves as a species
nonspecific mediator for entry of human and animal alpha herpesviruses
in a pathway independent of detectable binding to gD.";
Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                                                                                                                                                                                                                                                                                                16 LLRGPLLPRSFSGNPRALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                         OSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT
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                                                                                                                                                                                                                                                                                                                                           LLLFPLL--LFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS
                                                                                         TISSUE=Placenta;

ISOGAÍ T., Ota T., Niehikawa T., Hayashi K., Otsuki T., Sugiyama T., Sugaid T., Ota T., Niehikawa T., Hayashi K., Otsuki T., Sugaid S., Ishii S., Kawai Hio. Y., Salto K., Sugaid S., Ishii S., Kawai Hio. Y., Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO75105; BAC11404.1; --
GO; GO:0004872; F:receptor activity; IEA.
InterPro: IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09JKF6; 09ERL5; 09J117;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                  Eukaryofa, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                           Length 267;
                                                                                                                                                                                                                                                                                         42.6%; Score 1235; DB 2; Length 2
96.0%; Pred. No. 6.8e-84;
tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                    4F464A8A1BA0C451 CRC64;
  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 AA
          hypothetical protein FLJ90624.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                    267 AA; 29253 MW;
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                                                                                                                                                                                                                                                                                                      Local Similarity 96.0 es 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
01-OCT-2003 (TrEMBLrel.
Hypothetical protein FLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                    FROM N.A.
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                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                     SEQUENCE
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Poliovirus receptor related protein 1.

Extracellular (Potential).

Cytoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Poly-Glu.

Poly-Glu.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).
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PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
MEDLINE=20541977; PubMed=11090177;
DOI=10.1128/JVI.74.24.11773-11781.2000;
Shukla D., Dal Canton M.C., Rowe C.L., Spear P.G.;
"Striking similarity of murine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                    Zhan J., Wimmer E.; "MPRRI), a herpesvirus receptor, is expressed "Mouse nectin-1 (mPRRI), a herpesvirus receptor, is expressed floor plate during embryogenesis, suggesting a role in neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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MGD; MGI:1926483; Pvrll.
OCC: GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
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N-linked (GlCNAC...
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N -> D (in Ref. 1).
P -> PP (in Ref. 2)
S -> G (in Ref. 3).
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Pred. No. 1.6e-40;
                                                                                                                                                     alphaherpesvirus entry.";
J. Virol. 74:11773-11781(2000).
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EMBL; AF270977; AAF76195.1; -.
EMBL; AF297665; AAG22808.1; -.
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57064 MW;
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                                                                                                                                                                                                                                                                              STRAIN-Swiss Webster;
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                    22.5%; Score 653.5; DB 2; Length ilarity 32.3%; Pred. No. 4.4e-40; Conservative 83; Mismatches 176; Indels
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                                                                                                Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      57035 MW; A56FA2C7F8B25AFB CRC64;
                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                          EMBL, BOGGOGS4, AAHGOGS4.1; -... GO; GO:0005913; C:cell-cell adherens junction; IDA GO; GO:0005913; C:cell-cell adherens junction; IDA GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0005515; F:protein binding; IPI. GO; GO:0004872; F:receptor activity; IDA. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. InterPro; IPR003598; Ig. C. InterPro; IPR003596; Ig. V.
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                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6, TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 2.
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SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00406; IGv; 1.
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ses 169; Conserv
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SEQUENCE
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                                        X76400; CAA53980.2; ALT_INIT
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                                                                            AY029539; AAK33124.1;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-Daming, 18 Sequence=VSP_002624, VSP_002625; DISBASE: Defects in PVRL1 are a cause of cleft lip/palate-bisedcodermal dysplasia syndrome (CLPED1) [MIM:22500]. CLPED1 is ecrodermal dysplasia syndrome (CLPED1) [MIM:2500]. CLPED1 is dysplasia [MIM:255060] and Zlotogora-Ogur syndrome. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. MWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-95237621; Pubmed=7721102; DOI=10.1016/0378-1119(94)00842-G;
Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
Dubreuil P.;
"CDNA characterization and chromosomal localization of a gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with HSV glycoprotein D (gD).
SUBCELULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dysplasia.";
Nat. Genet. 25:427-430(2000).
-!- FUNCTION: Probably involved in cell adhesion. Receptor for
alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDILTB=20392366, PubMed=10932188; DOI=10.1038/78119; Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                            "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor."; Science 280:1618-1620(1998).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-98279152; PubMed-9616127; DOI=10.1126/science.280.5369.1618;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21256041; Pubmed=11356977;

DOI=10.1128/JVI.75.12.5684-5691.2001;

DOI=10.1128/JVI.75.12.5684-5691.2001;

Campadelli-Frjune G., Dubreuil P.;

Novel, soluble isoform of the herpes simplex virus (HSV) receptor excertal for prr1-HIGH-HVec) modulates positively and negatively susceptibility to hav infection.";

J. Virol. 75:5684-5691(2001).
   05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry
mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
                                                                            Name=PVRL1; Synonyms=HVEC, PRR1;
Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helms J.A., Spritz R.A.;
"Mutations of PVRL1, encoding a cell-cell adhesion
molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Alpha;
IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q15223-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM GAMMA).
                                                                                                                                                                                                                                                                                   to the poliovirus receptor gene.";
Gene 155:261-265(1995).
 05-JUL-2004 (Rel. 44,
                                                             antigen).
                                                                                                                                                     NCBI_TaxID=9606;
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-> KPRPORGLGSAARLLAGTVAVELILVAVLTVEDEDTVAVO
OKSPPETDGAGTDQPLSQKPEPSPSRQSSLVPEDIQVVHLD
PGRQQQGEEEDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Policovirus receptor related protein 1.
Extracellular (Potential).
Cycoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
Poly-Glu.
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By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
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N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
EFPYTPSFPEHGRAGPV -> AFCQLIYPGKGRTR.
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Receptor; Repeat; Signal; Transmembrane.
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/FIId=VSP_002624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005912; C:adherens junction; NAS.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0015025; F:correceptor activity; TAS.
GO; GO:0016337; P:cell-cell adhesion; NAS.
GO; GO:0006955; P:immune response; NAS.
GO; GO:0046718; P:viral entry; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 2.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Alternative splicing; Cell adhesion; Glycoprote
Immunoglobulin domain; Receptor; Repeat; Signal
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EMBL; AF252867; AAC16648.1; EMBL; AF196768; AAC16648.1; JOINED. EMBL; AF196769; AAC16648.1; JOINED. EMBL; AF196770; AAC16648.1; JOINED. EMBL; AF196771; AAC16648.1; JOINED. EMBL; AF196774; AAC16649.1; JOINED. EMBL; AF196769; AAC16649.1; JOINED. EMBL; AF196770; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC1649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED. EMBL; AF196772; AAC16649.1; JOINED.
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Best Local Sim.
Matches 170;
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TRANSMEM
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                                                                                                                                                                                                                                       RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKS 302
                                                                                                                                                                                                                        VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTT 362
                                                                                                                                                                                                                                                                    TLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVL 422
                                                                                                                                                                                                                                                                                    AGIF--CYRRRIFRGDYFAKNYI-------PPSDMQKESQIDVLQQDELDSY 466
                                                                                                                                                                                                                                                                                                                                                            PDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN--------VENLNRPE 505
                                                                                                                                                                                                                                                                                                                                                                                 PDDSDDEKKAGPLGG---SSYEBEBEBEGGGGGERKVGGPHPKYDEDAKRPYFTVDEAE 475
                                                                                                FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG
                                                                                                                                            SLACIVNYHM--DRFKESLTLNVQYEPEVTIEGFDGNWYLQRMDVKLTCKADANPPATEY
                                         GKNVSLKCLIE --- VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                         128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is a functional alphaherpesvirus receptor.";
Virology 281:315-328(2001).
-!- FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorables virus) entry into
                                                                                                                                                                                                                                                                                                                                       GGIVVALRRRRHTFKGDYSTKKHVYGNGYSKAGIPQHHPP--MAQNLQ------Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBGNIT: Interacts with HSV glycoprotein D (gD) (By similarity) SUBGELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                         549
                      Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       RPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
                                                                                                                                                                                                                                                                                                                                                                                                                      ARQDGYGDRTLGYQY--DPEQLDLAENWVSQNDGSFISKKEWYV
          Pred. No. 8.7e-40;
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31.9%; F1.
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
          Similarity
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                      167;
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ong as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%; Score 641.5; DB 1; Length 515; 32.0%; Pred. No. 3.4e-39;
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                                                                                                                                                                                                                                                                                                     Potential.
Poliovirus receptor related
Extracellular (Potential).
Cytoplasmic (Potential).
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Ig-like C2-type 1
Ig-like C2-type 1
Ig-like C2-type 2
Poly-Glu.
Poly-Glu.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc.
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use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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                                                                                                          EMBL; AF308632; AAG30281.1; -.
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                                                                                                                                                InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig_v.
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                                                                                                                                                                                                                                                                                 Signal; Transmembrane
SIGNAL 1
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515 AA;
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                                                                                                                              HSSP; Q05793; 1GL4
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151 VIFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDL 210
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PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein FLJ14847.
Homo sapiens (Human).
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Q96K15;
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A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Ehat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,
A Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Halton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halton B.K., Muzny D.M., Garen E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.,
Brodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Brons S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=21560925; PubMed=11544254; DOI=10.1074/jbc.MI03810200; Reymond N., Fabre S., Lecoqg E., Adelaide J., Dubreuil P., Lopez M.; "Nectin4/PRR4, a new afadin-associated member of the nectin family that trans-interacts with nectin1/PRR1 through V domain interaction."; J. Biol. Chem. 276:43205-43215(2001).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                498 VENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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    Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                          Created)
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Pfam; PP00047; ig; I.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 510 AA; 55454 MW;
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149; Conserv
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05-JUL-2004
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RA CLEARLY SUZUKI, Y. NISHIKAWA T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamaten A., Hayashi W., Nishi T., Shibahara T., Tanaka T., Ishibahara T., Tanaka T., Ishibahara T., Tanaka T., Ishibi S.,
RA Sekine M., Obeyashi M., Nishi T., Shibahara T., Tanaka T., Ishib S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Magatsuma M., Shiratori A.,
RA Garama K., Kamihara K., Kateuta N., Sato K., Tanikawa E., Omura Y.,
RA Takahashi M., Kateuta N., Sato K., Tanikawa E., Omura Y.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Natani H., Yakanabe M., Hara H., Tanase T., Nomura Y.,
RA Kanehori K., Takabashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Kanehori K., Takabashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Masashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Noshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Wamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami T.,
RA Marazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami Y., Oh, T., Yamada K., Fujii T., Kobatake N., Inagami A., Pujiwara T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa R.,
RA Nakagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakagase T., Shitai Y., Takahashi Y., Nakagawa K.,
RA Nakagano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa K., Shitai R., Nakagase T., Nomura N., Kikuchi H., Masuho Y., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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                               187
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130 STFPAGSFÇARLRIRVLVPPLPSLNPGP-ALEEGGGLTLAASC-TAEGSPAPSVTWDTEV
                                                                                                                                                                                               389 PPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRRTFRGDYFAKNYIPPSD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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151 VTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDL 210
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 "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                             Length 510;
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18.7%; Score 543; DB 2; Length 510
Best Local Similarity 28.4%; Pred. No. 7.6e-32;
Matches 149; Conservative 85; Mismatches 213; Indels
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                            Mat. Genet. 36:40-45(2004).

EMBL, AK027753; BAB55344.1; -.

GO; 00004872; F:receptor activity; IEA.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003598; Ig_c2.

Ffam; PR0047; ig_1.

PROSITE; PS50835; IG_LIKE; 3.
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Sequence 4, Appli
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Copyright (c) 1993 - 2005 Compugen Ltd
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Sequence Sequence Sequence Sequence

Sequence Sequence

4 US-09-909-064-84 Sequence 84, Appl 4 US-09-905-381A-84 Sequence 84, Appl 4 US-09-906-618-84 Sequence 84, Appl 4 US-09-906-618-84 Sequence 84, Appl 4 US-09-9078-510-2 Sequence 2, Appl 5 Sequence 917, Appl 1 US-09-915-524-19 Sequence 917, Appl 3 US-09-915-524-19 Sequence 19, Appl 4 US-09-915-524-19 Sequence 19, Appl 4 US-09-949-016-11044 Sequence 11044, Appl 1 US-09-949-016-110547 Sequence 11044, Appl 1 US-09-949-016-6213 Sequence 7850, Appl 4 US-09-949-016-7850 Sequence 7850, Appl 2 US-09-949-016-7850 Sequence 7850, Appl 3 US-08-949-016-7850 Sequence 7850, Appl 2 US-08-949-016-7850 Sequence 7850, Appl 2 US-08-949-016-7850 Sequence 7850, Appl 2 US-08-949-016-7850 Sequence 7850, Appl 2 US-08-949-016-7850 Sequence 7850, Appl 2 US-08-948-2 Sequence 3, Appl 3 US-08-948-2 Sequence 3, Appl 3 US-08-684-594-3 Sequence 3, Appl 3 US-08-948-2 Sequence 3, Appl 3 US-08-986-594-3 US-08-986-594-3 Sequence 3, Appl 3 US-08-986-584-594-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-584-3 US-08-986-98-98-98-98-98-98-98-98-98-98-98-98-98-	AL: 99499 al. D1S1 D1S1 4, 755 7, 766 1, 498	4%; Score 649.5; DB 4; Length 514; 9%; Pred. No. 1e-51; 80; Mismatches 182; Indels 95; Gaps 17	GKNVSLKCLIEVNETITQISMEKIHGKSSQIVAVHHPQYGFSVQGEYQGRULFKNYS 127	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG 184	FATFPTGNRESQLNLTVMAKPT-NWIEGTQ	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR 242 ::: : : : QDDKVLVATCTSANGKPPSVVSWETRLKGBAEYQEIRNFNGTVTVISRYRLVPSREAHQQ 219	SFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANDPFKS 30	GNWYLQRMDVKLTCKADANPPATEY 27	VWSKLDGQWPDGLAASDNTLHKVMPLTFWRSGVILCKVTNSLGQRSDDQKVIXISDFTTT 362 	SVL 42
8.4 398 8.6 4 398 8.0 4 432 7.5 6.6 6.6 5 227 6.5 227 6.5 227 6.3 819 6.3 819 5.8 1709 5.7 477		22.4%; larity 31.9%; Conservative	GKNVSLKCLIEV : GTDVVLHCSFANPLE	ATITTHNIGFSI	GTIRLSRLELEI	ETVAAICIAATC : : : KVLVATCTSANC	TCVVKHPALEKDIRY	SLACIVNYHMDRFKE	RLDGOWPDGLLA 	PTIQWHPSTADI
2433 2433 2433 2433 2433 2433 1800 1800 1807 1807 1807 1807 1807 1609 1609 1609 1609 1609 1609	SULT 1 -09-949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380 -949-016-11380	/ Match Local Similarit les 167; Conse	71 GKN : 41 GTD	128 LND	101 FTDC	185 -GNJ 160 QDDJ	43 RI :	200	303 VWSP 	63
	RESULT 1 US-09-949- Sequence Sequence FREENL TITLE TITLE TITLE TITLE CURRENT CURRENT CURRENT CURRENT FRIOR F F FRIOR F F F F F F F F F F F F F F F F F F F	Query Ma Best Loc Matches	& 8	ò	Д	දු පු	Š	a :	장 쉽	ò

	FISKKEWYV 51	; GENERAL INFORMATION: ; APPLICANT: Faris, Mary ; APPLICANT: Turner, Christopher M. ; TITLE OF INVENTION: PROSTATE CANCER WARKERS ; FILLE REFERENCE: PA-0036 US ; CURRENT APPLICATION NUMBER: US/09/919,172 ; CURRENT FILLING DATE: 2001-07-30 ; PRIOR APPLICATION NUMBER: 60/222,469 ; PRIOR PILING DATE: 2000-07-28	NUMBER OF SEQ ID NOS: 102 SOFTWARE: PERL Program SEQ ID NO 20 LENGTH: 518 TYPE: PRT ORGANISM: Homo sapiens FBATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1	Query Match 21.6%; Score 627; DB 4; Length 518; Best Local Similarity 30.8%; Pred. No. 1.3e-49; Indels 112; Gaps 18; Matches 164; Conservative 80; Mismatches 177; Indels 112; Gaps 18; QY 71 GKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSVQSFYQGFVLFKNYS 127	Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBETVSLIKGFDSLIDG 184 : :	Qy 185 -GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKL 233	Qy 234 FPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNA 293	Qy 294 DANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVICKVTNSLGQRSDQKVI 353	Qy 354 YISDPPTTTLQPTIQWHPSTADIBDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGA 413	PPSDMQKESQIDV 	Qy 458 LQQDELDSYPDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN 497
:	Cy SOG KPMINIANGERINGS OF STANDERS OF STAN	O	200000	(2)	Query Match 22.4%; Score 649.5; DB 4; Length 517; Best Local Similarity 31.9%; Pred. No. 1e-51; Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;	Qy 71 GKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNVS 127 	Qy 128 INDATITHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGFDSLIDG 184	Qy 185 -GNETVAALCIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR 242 ::: : : : : : : :	Qy 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKS 302 223 SLACIVNYHMDRFKESLTLNVQYEPEVTIEGFDGNWYLQRMDVKLTCKADANPPATEY 280	Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTT 362 	, Oy 363 TLQPTIQWHPSTADIEDLATEPKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVSVL 422

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 IIVEPHVTAVWGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFSVQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VTVLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHI------DWEGDL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 NYSGVYIÇKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSV 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------RGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPVNNL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RPPQSGPRASGRAQSPPGPSMARAAALLPSRSPPTP-----LLWPLLLLLLLETGAQDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 VQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 RPSPLCP-GGGKAQL-SSASLLGAGLLL---QPPTPPPLLLLLFPLLLFSRL-CGALAGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 469.5; DB 4;
26.0%; Pred. No. 6.8e-35;
ive 78; Mismatches 199;
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                                               Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.0%
Matches 158; Conservative
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                                                 Sequence 7563, Applic
patent No. 6812339
GENERAL INFORMATION:
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APPLICANT: Universita degli Studi di Bologna
APPLICANT: Institut National de la Sante et de la Recherche M
TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
TITLE OF INVENTION: BHV Infections
FILE REFERENCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
CURRENT PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
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128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
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OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
OTHER INFORMATION: Superfamily
OTHER INFORMATION: Binding Macromolecules: HSV-gD
OTHER INFORMATION: Subcellular localisation: Plasma Membrane
OTHER INFORMATION: Other Information: Viral Receptor
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                                                                                                   PYFTVDEAEARQDGYGDRTLGYQY--DPEQLDLAENWVSQNDGSFISKKEWYV
                                                                        -VENLINRFERPMDYYEDLKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
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                                                                                                                                                                                                                                     Sequence 1, Application US/09435956A Patent No. 6469155 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 148; Conserv
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                                                                                                                                        APPLICANT: NORTHWESTEN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARTHWES, Morgyn S.
APPLICANT: WARTHWES, Wanda M.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: COHEN, Gary H.
APPLICANT: COHEN, Gary H.
APPLICANT: WHITHECK, Charles J.
APPLICANT: KRUMMENACHER, Claude
APPLICANT: KRUMMENACHER, Claude
APPLICANT: WHITHECK, Charles J.
APPLICANT: WHITHER, Claude
APPLICANT: WHITHER, Claude
APPLICANTON: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290.0050/201
CURRENT FILING DATE: 2009-11-28
PRIOR PELLOATION NUMBER: U.S. 60/087,862
PRIOR PELLOATION NUMBER: U.S. 60/087,862
PRIOR PELLOATION NUMBER: PCT/US99/12235
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PRIOR PELLOATION NUMBER: PCT/US99/12235
PRIOR PELLOATION NUMBER: 1998-06-02
SOFTWARE: PATERIL VAT. 2.1
FENOTH: APPLICATION NUMBER: PCT/US99/12235
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25.7%; Pred. No. 2.4e-34;
Live 76; Mismatches 184; Indels 169;
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                                                                        ; Sequence 2, Application US/09723368; Patent No. 6641818; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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JAPELICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSELSEQ for Windows Version 4.0

LENGTH: 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PPTP----LLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHILLPPVPGLYISL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 PPTPPPLLLLLEPLLLESRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR
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                        514 LKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 549
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25.7%; Pred. No. 2.4e-34;
tive 76; Mismatches 184
514 LKMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
                                                                                                                                                     US-09-949-016-6278
Sequence 6278, Application US/09949016
; Patent No. 6912339
; GENERAL INFORMATION:
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336 KP--ENMOONTRLHL-----
                                                                                                                                                                                     Best Local Similarity 20.03
Matches 134; Conservative
                                                                                                                                                                                  Similarity
                                                                                                                 ; ORGANISM: Mouse US-09-724-864-62
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ORGANISM: Human
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                                                                                  LENGTH: 408
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Best Local S
                                                                                                 TYPE: PRT
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   GRUERCE 7564, Application US/09949016

FREED NO. 681239
GENERAL INFORMATION:
FREED TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REPERENCE: CL001307
CURRENT FILING DATE: 2000-10-20
FRIOR PRIOR PLING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESE OF Windows Version 4.0
SEQ ID NO 7564
LENGTH: 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 LIEVNET----ITQISWEKIHGKSSQTVAVHH----PQYGFSVQGRYGRVLFKNYSLNDA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 VKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRL 307
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Patent No. 6380362
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
James D
APPLICANT: Watson, James D
APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
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                                                                                                                                                                                                                                                                                                                                                                                                       13.6%; Score 394.5; DB 4; Length 27.8%; Pred. No. 5.6e-28; tive 69; Mismatches 174; Indels
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Best Local Similarity 27.8'
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human
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US-09-949-016-7564
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US-09-724-864-62
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Sequence 6729, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT PILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 6729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLI--DG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 GNETVAAICIAATGKPVAHIDW----EGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                       13.5%; Score 391; DB 3; Length 406
28.0%; Pred. No. 9.8e-28;
ative 71; Mismatches 178; Indels
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
NUMBER: 0F SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
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P--TIPP-----PTTTTTTTTTTTT------TTTILTIITDSRAGEEGSIRAVDHAVIG 378
187 ETVAAICIAATGKPVAHIDW-EGDL-----GENESTITSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDP
                                                                           241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVT
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                                                                                                                                                                                                                                                                                                              412 GALFIVLVSVLAGIFCYRRRRTFRGDYFAKN 442
                                                                                                                                                                                                                                                                                                                                     379 GVVAVVVFAMLCLLI-----ILGRYFARH 402
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09930803
Patent No. 6596493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 442
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 YPPEVGISGYDNNWYLGQNEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL-LIR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
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                                                                                                                                                                                                                                    -HGESGSMAVFHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLF 125
                                                                                                                                                                                                                                                                        VIPPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
                                                                                                                                                                                                                                                                                                DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                         DLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGRAVTCKVEHESFEKPQLLTVNLTVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                               YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 386
                                                                                                                                                                                              IHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK
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                                                                                 61;
                                           Length 417;
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                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PSEHSGMSR-----NAIIFLVLGILVFLILLGI--GIYFY 366
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                                         13.5%; Score 390.5; DB 4; 27.6%; Pred. No. 1.1e-27; ive 68; Mismatches 162;
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TITLE OF INVENTION: Molecules Designated
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1990-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 25.55
Matches 115; Conservative
                                                                                 111; Conservative
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                                                               Similarity
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     JS-09-949-016-6729
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US-09-778-510-20
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                                           Query Match
Best Local S
Matches 111
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, Roger
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REPERENCE: JHUJ770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32 18; 358 187 ETVAAICIAATGKPVAHIDW-EGDL-----GEMESTITISFPNETATIISQYKLFPTRFAR 240 334 P--TIIPP-----PTTTTTTTTTT------TTTLLIITDSRAGEEGSIRAVDHAVIG 378 103 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPP 298 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDP 358 PITITLOPTIOWHPSTADIEDLATEPKKLPFPLSTLATI------KDDTIATIIASVVG 411 PITITLQPIIQMHPSTADIEDLATEPKKLPFPLSTLATI-----KDDTIATIIASVVG 411 68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127 128 INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGN 186

373 AVIGGVVAVVVPAMLCLLI-----ILGRYFARH 400

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412 GALFIVLVSVLAGIFCYRRRRTFRGDYFAKN 442

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2006-067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/074,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/146,222
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Sequence 61, Application US/0994457
Patent No. 6734288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: December 12, 199 APPLICATION NUMBER: 60/069,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/069,87
FILING DATE: December 17, 199
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                                                                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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                                                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
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                                                                               Baker, Kevin
Botstein,David
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Hillan, Kenneth
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                                                                                                                                                                                                                                                                                                                                                               Kljavin, Ivar
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                                                                                                                                                                                                                                                                                                                                                                                         Napier, Mary
                                                                                                                                      Eaton, Dan
                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 LNFSSSELKVSLINVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAV 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFRENCE: P25.49PILC.
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120 SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.5%; Score 333.5; DB 4; Length 4 Best Local Similarity 25.7%; Pred. No. 2.6e-22; Matches 117; Conservative 85; Mismatches 176; Indels
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                                                  Sequence 61, Application US/09866028 Patent No. 6642360
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Grimaldi, Christopher
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Filvaroff, Ellen
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Botstein, David
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ORGANISM: Homo Sapien
                                                                                                                                                                                Eaton, Dan
                                                                                               GENERAL INFORMATION:
                     -09-866-028-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 DGGNETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETAŢIIŞQYKLFPT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 RFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNAD 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALA----GPIIVE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SVVLPSGSQCAAAAA-----AAPPGLRLL---LILFS--AAALIPTGDGQNLFT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 KDVTVIEGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQL 97
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                    PILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MARCH 3, 1999
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: JUNE 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR FILING DATE: NO. 6734288ember 30, 1999
OR FILING DATE: NO. 6734288ember 30, 1999
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: December1, 1999
OR APPLICATION NUMBER: PCT/US99/28301
OR PELLING DATE: December1, 1999
OR APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                        TELING DATE: December 16, 1999
OR APPLICATION NUMBER: PCT/US00/03565
OR FILING DATE: Pebruary 11, 2000
OR APPLICATION NUMBER: PCT/US00/04414
OR FILING DATE: Pebruary 22, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: May 22, 2000
OR FILING DATE: May 22, 2000
OR FILING DATE: May 22, 2000
OR FILING DATE: May 22, 2000
OR FILING DATE: July 28, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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Best Local Similarity 25.77
Matches 117; Conservative
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 APEVSVTGYDGNWFVGRKG--VNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 HPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 KLPFPLSTLATI-----KDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 HGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PPGLRLRLLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISC--QVNKSDDSVI--QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 LGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGNETVAAICIAATGKPVAHIDW-EGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP--TTIPP----PTTTTTTTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 PPPL-LILLEPLILESRICGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 325.5; DB 4; 26.2%; Pred. No. 1.4e-21; ive 79; Mismatches 175;
                                                                                                                 Molecules Designated B7L1
                                                                           GEMERAL.

JITLE OF INVENTION: Molecules Designate.
FILE REFERENCE: 2844-US
CURRENT PELLION NUMBER: US/09/778,510
CURRENT PELLING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22.
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BER: PCT/US99/17906
1999-08-05
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US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095;
; GENERAL INFORMATION:
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LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
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Sequence 15,
Sequence 13,
Sequence 12,
Sequence 10,
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Sequence 2, A
Sequence 2, A
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22: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-161-572-45
US-09-972-268-4
US-09-972-268-2
US-09-972-268-17
US-09-972-268-15
US-09-972-268-13
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Sequence 8, Appli
Sequence 14, Appl
Sequence 16, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 2626, Appli
Sequence 20, Appli
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Sequence 21, A
Sequence 5, Al
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0. US-09-972-268-8

0. US-09-972-268-14

0. US-09-959-845-6

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649.5
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ALIGNMENTS

; Sequence 6, Application US/09972268; Publication No. US20030044893A1; Sequence 6, Application No. US20030044893A1; Bublication No. US20030044893A1; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.; APPLICANT: Forton, Timothy E.; APPLICANT: Sorensen, Eric A.; APPLICANT: Sorensen, Eric A.; APPLICANT: Youakim, Adel; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TI; TITLE OF INVENTION NUMBER: US/09/972,268; CURRENT APPLICATION NUMBER: US/09/972,268; PRIOR FILING DATE: 2000-10-05; PRIOR FILING DATE: 2000-10-05; NUMBER OF SEQ ID NOS: 39; SOFTWARE: Patentin version 3.1; SEQ ID NO 6; LENGTH: 549 Query Match 100.0%; Score 2901; DB 10; Length 549; Best Local Similarity 100.0%; Pred. No. 1.5e-214; Matches 549; Conservative 0; Mismatches 0; Indels 0; TYPE: PRT ORGANISM: homo sapiens US-09-972-268-6

9 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI Gaps ; 0

IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120

61

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360

420

420

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240 240 300

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540 540

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Sequence 4, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Fanslow, William C.

APPLICANT: Inchion, Timothy E.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Exic A.

APPLICANT: Sorensen, Exic A.

APPLICANT: Solution NUMBER: US/09/972,268

CURRENT APPLICATION NUMBER: US/09/972,268

CURRENT APPLICATION NUMBER: 60/238,557

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fro OTHER INFORMATION: m human Nectin-3 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                                                                             181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                                                                                                                                                                                                                   361 TTTLQPIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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99.5%; Score 2887; DB 10;
Best Local Similarity 99.6%; Pred. No. 1.8e-213;
Matches 547; Conservative 0; Mismatches 2;
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CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2002-02-15
PRIOR PILING DATE: 2002-02-15
PRIOR PILING DATE: 2002-02-15
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    61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                           VLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                  VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                        LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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100.0%; Pred. No. 1.5e-214;
live 0; Mismatches 0;
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US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
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Matches 549; Conservative
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ORGANISM: Homo sapiens
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121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEFTVSLIKGPDS 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEFTVSLIKGPDS 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEFTVSLIKGFDS 181 LIDGGNETVAAICITAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 181 LIDGGNETVAAICITAATGKFVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF	OY 301 ASVARIAGEMENTAL THE VHELTENIS OF TEXT TO ASSAULT 1500 FOR ASVARIANCE ASSAULT AS AS ASSAULT AS AS AS AS AS AS AS AS AS AS AS AS AS	QY 421 VLAGIPCYRRRTFRGDYFAKNYIPPSDWQKESQIDVLQQDELDSYPDSVKKENKNPVNN 480 DD 421 VLAGIPCYRRRTFRGDYFAKNYIPPSDWQKESQIDVLQQDELDSYPDSVKKENKNPVNN 480 QY 481 LIRKDYLEEPEKTQWNNVENLANFPERPWDYYEDLKWGWKFVSDEHYDENEDDLVSHVDGS 540 DD 481 LIRKDYLEEPEKTQWNNVENLANFPERPWDYYEDLKWGWKFVSDEHYDENEDDLVSHVDGS 540	Cy 541 VISREENTY 549 Db 541 VISREENTY 549 ERSULT 4 (B-09-2-268-2	Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNE 187 Db 121 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNE 180

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US-09-972-268-15

US-09-972-268-15

Sequence 15, Application US/09972268

Publication No. US2030044893A1

Sequence 15, Application US/09972268

Publicant USCOMMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Lofton, Timothy E.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Adel

TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE REFERENCE: 3101-A

CURRENT APPLICATION NUMBER: US/09/972,268

CURRENT FILING DATE: 2001-10-05

PRIOR FILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 15:

LENGTH: 426
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241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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Publication No. US20030044893A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Banslow, William C.
APPLICANT: Fanslow, William C.
APPLICANT: Cofenon, Timothy E.
APPLICANT: Corensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE OF INVENTION NUMBER: US/09/972,268
CURRENT PAPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
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   181 LIDGGNETVAAVCVAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTRFAR 240
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ORGANISM: mus musculus
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US-09-972-268-17
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APPLICANT: Fanelow, William C. APPLICANT: Fanelow, William C. APPLICANT: Sorensen, Eric A. APPLICANT: Sorensen, Eric A. APPLICANT: Sorensen, Bric A. APPLICANT: Sorensen, Bric A. TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A CURRENT APPLICATION NUMBER: US/09/972,268 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR PILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin version 3.1 SEQ ID NO 12 LENGTH: 510
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66.2%; Score 1920.5; DB 198st Local Similarity 67.9%; Pred. No. 4.4e-139;
Matches 390; Conservative 33; Mismatches 62;
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US-09-972-268-10
Sequence 10, Application US/09972268
Sequence 10, Application Wolvey 1
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
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US-09-972-268-12
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Sequence 13, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanshow, William C.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youskim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A
CURRENT FILING DATE: 2001-10-05
FRIOR APPLICATION NUMBER: 60/238,557
PRIOR PLILING DATE: 2000-10-05
PRIOR PLILING DATE: 2000-10-05
SOFTWARE: Patentin version 3.1
SEQ ID NO: 3
SEQ ID NO: 3
ENGINE SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE ABOUT SACE A
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US-09-972-268-13
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ilarity 99.5%; Pred. No. 2.6e-154;
Conservative 0; Mismatches 2;
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US-09-972-268-12
'Sequence 12, Application US/09972268
'Publication No. US20030044893A1
'GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Sequence 8, Application US/09972268;
Sequence 8, Application US/09972268;
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
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APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: 
         TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF MAKING AND USE TR
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                                FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
FRIOR APPLICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 437
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
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APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
FILE RERERBINCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
TENGTH: 510
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 67.6%; Pred. No. 5.3e-138;
Matches 388; Conservative 33; Mismatches 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-972-268-31
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanelow, William C.
APPLICANT: Sorensen, Bric A.
APPLICANT: Sorensen, Bric A.
APPLICANT: Sorensen, Bric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T FILE REFERENCE: 310.1-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 00/138,557
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
SOFTWARE: PATENT NOWER OF SEQ ID NOS: 39
SOFTWARE: PATENT NO VERSION 3.1
SEQ ID NO 16
LENGTH : 387
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  65.1%; Score 1889; DB 10; 76.0%; Pred. No. 1.5e-136; tive 16; Mismatches 72;
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Best Local Similarity 98.3%; Pred. No. 5.6e-136;
Matches 357; Conservative 0; Mismatches 6;
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
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                                             Conservative
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381; Conserv
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APPLICANT: Baum, Peter R.
APPLICANT: Fanelow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Soremsen, Eric A.
APPLICANT: Soremsen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-110-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 595
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                                                                                                                                                1 PSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLFFPLLLFSRLCGALAGPIIVEPHV 60
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                                          DB 10; Length 504;
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                                                                                 62; Indels
                                      tch 65.2%; Score 1892.5; DB 3
al Similarity 67.6%; Pred. No. 6.2e-137,
384; Conservative 33; Mismatches 62,
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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  JS-09-972-268-8
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384 VFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPVVEERIPSLPQKDLLGQTEHLPLQTQF
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Job time : 257.269 secs
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                                  61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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62.5%; Score 1814.5; DB 1C
Best Local Similarity 66.4%; Pred. No. 6.4e-131;
Matches 374; Conservative 39; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Keriko SATO
APPLICANT: Keriko SATO
APPLICANT: Keriko SATO
APPLICANT: Keriko SATO
AURENT: REPERBENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT PILING DATE: 2001-12-31
PRIOR FILING DATE: 2001-13-09
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VOICES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09959845
Publication No. US20030008334A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Mouse
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US-09-959-845-4
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US-09-959-845-4
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Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.
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/.ore= "Mouse nectin-3 pprotein"
7. .510
/note= "Human nectin-3beta protein"
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N-PSDB; AAD37444.
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Lofton TE,

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Interitual relates to a subscontrainty pullibron incoming in related.

The interitual relates to a subscontrainty pullibron and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function discribing activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, cedema, diabetto retinopathy asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modularing proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein encoding 6 manno acide from mouse nectin-3 protein and the rest form human nectin-3 beta protein. Human nectin-3 protein allocated on chromosome 3.

(Updated on 29-NUG-2003 to standardise OS field)
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Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3. Youakim A; /note= "Intracellular C-terminal domain" 'note= "Extracellular Ig domain" 74. .152 /note= "Extracellular Ig domain" domain" Sorensen EA, /note= "Extracellular Ig /note= "N-glycosylated" 189. .250 /note= "N-glycosylated" note= "N-glycosylated" 'note= "N-glycosylated" /note= "N-glycosylated" /note= "N-glycosylated" Location/Qualifiers Lofton TE, 05-OCT-2001; 2001WO-US031392. 05-OCT-2000; 2000US-0238557P Human nectin-3beta protein. .510 Fanslow WC, 287. (IMMV) IMMUNEX CORP. WPI; 2002-426103/45. 186 N-PSDB; AAD37445 WO200228902-A2 Modified-site Modified-site Modified-site Modified-site Modified-Bite Modified-site Homo sapiens 11-APR-2002 Baum PR, Domain Domain Domain Domain

WPI; 2002-426103/45. N-PSDB; AAD37445. Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

Claim 1; Page 98-99; 141pp; English.

sepsis, stroke

The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial cor endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or migration distributed method is inflammation, sepsis, cedema, diabetic retinopathy, astendial barrier function disorder which is treated by the above mentioned method is inflammation, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for not inflammatory bowel disease. Nectin DNA is also useful for proliferation or angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenesis, ischaemia-repertusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothalial cell, an epithelial cell or a smooth muscle cell). The present sequence is human nectin-Jabeta protein.

AAE23286 standard; protein; 510 AA

RESULT 2 AAE23286 (first entry)

27-AUG-2002

AAE23286;

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Matches 504;
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                                                                                 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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                                  Score 2693; DB 5;
Pred. No. 2.3e-215;
0; Mismatches 2;
gene is located on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human deleted nectin-3beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE23284 standard; protein; 504
                                  99.3%;
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                                          Best Local Similarity 99.6
Matches 508; Conservative
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Human nectin-3beta
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                  Sequence 510
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The inversion contracts to a subcanniant purified medical solutions of gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corrections activity, epithelial partier function disorder which is treated by the above motherial barrier function disorder which is treated by the above mentioned method is inflammation, soems, odema, diabetic retinopathy, astraction of inflammation, soems, odema, diabetic retinopathy, astraction of inflammation, some manness in cancer cells, astraction or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as inschaemia, atheroselerosis, is chaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an smooth muscle cell). The present sequence is human nectin-labeta protein containing 6 amino acids deleted from the N-terminal end. Human nectin-labeta protein.
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                                                                                                                                                       purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
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                                                                                                                                                                                    useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy,
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Youakim
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Pred. No. 3.2e-214;
Sorensen EA,
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100.0%; Pred
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Fanslow WC,
                                                              2002-426103/45.
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The invention relates to a substantially purified nectin3alpha, beta, command and nectin-4 polypeptides and their corresponding polynucleotides. Command and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherns function formation activity, epithelial corresponding nativity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, condition of a tissue or a subject, such as including angiogenesis, tumour growth and treating herpesvirus infection. Stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular
                         301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQKVIYISDIPL 360
                                                                                                            361 TQTSSIAVAGAVIALFIITVFVTVL/LTPRKKRPSYLDKVIDLPPTHKPPVYEERI 420
                                                                                                                                                                                                  Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, nectin-3beta, therapy, cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allergy; allegate rejection; metastasis; restenosis; inflammatory bowel disease; ocdema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                     KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS
                                                                                                                                                                           PPLPQKDLF-QPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorensen EA,
                                                                                                                                                                                                                                                                                          NOMCYQDRSPGKHHQNNDPKRVYIDPREHYV 510
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                                                                                                                                                                                                                                                                                                                                                                                                                            Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse nectin-3beta protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR 120
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                                                                                                                                                                                                                                                                                          Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iagnosing and treating tumor infiltration and mouse nectin-3 protein families and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLLFPLLLFSRLCGALAGPI
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89.2%; Pred. No. 1.9e-191;
ive 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato K;
                                                                                                                                                                                                                                                Amino acid sequence of murine nectin-3,
  RSPGKHHQNNDPKRVYIDPREHYV 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISC-) JAPAN SCI & TECHNOLOGY CORP. (TAKA/) TAKAHASHI K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment and prevention of cancer
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                                                                                                               AAG63983 standard; protein; 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39-MAR-2001; 2001WO-JP001871
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Matches 456; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastaais; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
 The present sequence is mouse nectin-3beta protein
                                                                                                                             IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR
                                                                                                                                                                                                          1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLLFPLLLFSRLCGALAGPI
                                                                                       IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                        VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                                      88.7%; Score 2406; DB 5;
89.2%; Pred. No. 1.9e-191;
ive 22; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                        Matches 456; Conservative
smooth muscle cell).
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                                               Similarity
                    Sequence 510 AA;
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Gamma and nectin-4 polypeptides and their corresponding polymuclectides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding but the endothelial proliferation or endothelial barrier function activity. The endothelial proliferation or endothelial barrier function disorder which is treated by the above cendothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, ocdema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, correct in transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, setroke, restenosis, isohaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

Shotin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3gamma protein.
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                                                                                                                                                                  purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGGRSDQKVIYISDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a substantially purified nectin3alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                          useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 437;
   Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2243; DB 5;
Pred. No. 5.8e-178;
0; Mismatches 2;
Sorensen EA,
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 125-126; 141pp; English.
   Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.7%;
larity 99.5%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430
                                                                    WPI; 2002-426103/45.
N-PSDB; AAD37450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLPQKDLFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 428; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 437 AA;
                                                                                                                                                                                                                                                                           sepsis, stroke
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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or endothelial barrier function activity, endothelial proliferation or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration.
Mouse; nectin-1gamma; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is mouse nectin-3gamma protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel purified nectin-3 and nectin-4 polypeptides which bind tuseful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 111-112; 141pp; English.
                                                                                                                                                                                                                            AAE23293 standard; protein; 438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2001; 2001WO-US031392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2000; 2000US-0238557P
                                                                                                                                                                                                                                                                                                                                                            Mouse nectin-3gamma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                    428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-426103/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                      PPLPQKDL
                                                                                                               PSLPOKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200228902-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sepsis, stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                 27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQRVIYISDIPL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTITSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDGGNETVAAVCVAATGKPVAQIDWEGDLGEMESSITSFPNETATIVSQYKLFPTRFAR
                                                                                                                                                                                 Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ķ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato
                                                                                                                                        Amino acid sequence of murine nectin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakanishi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 53-55; 64pp; Japanese.
      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment and prevention of cancer
      AAG63984 standard; protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                JAPAN SCI & TECHNOLOGY TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                            09-MAR-2001; 2001WO-JP001871.
                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2000; 2000JP-00065595
                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi K, Takai Y,
                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-570771/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 438 AA;
                                                                                                                                                                                                                                                                     WO200166736-A1.
                                                                                             26-NOV-2001
                                                                                                                                                                                                                                                                                                                   13-SEP-2001
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Best Local {
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                                                  AAG63984
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The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adensely ilunction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthery, allograft rejection, meteateasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, condition of a tissue or a subject, such as ischaemia, atherosalarosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour giveth and treating herpeaviers infection.
                                                                                                                                                                                                                                                                                                                                                                                    Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.3
Best Local Similarity 86.8
Matches 375; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2002
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LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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  Length 595;
                                                          Indels
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71.3%; Score 1932; DB 5;
86.8%; Pred. No. 7.6e-152;
tive 3; Mismatches 16;
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 atherosclerosis; ischaemia-reperfusion injury; thrombosis; tumour; cancer; herpesvirus infection; fusion protein; asthma.
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/note= "Human nectin-3alpha protein"
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382. .387
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Best Local Similarity 100.
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Baum PR, Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                 (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-426103/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sepsis, stroke.
                                                                                                                                                                                                                                                           WO200228902-A2
                                                   Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                              11-APR-2002
                                                                                   Chimeric.
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oedema;
                     stroke;
                                                                                                                                       Region
                                                                                                                                                                         Region
                                                                                                                                                                                                           Region
                                                                                                                         Key
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300
                                                                                                                 360
181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                              300
                                                                                                                                   301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; cedema; atherosclerosis; ischaemaia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or
                                                                241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                             GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Human nectin-3alpha protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse nectin-3-human nectin 3alpha fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Mouse nectin-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 80-82; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                           AAE23282 standard; protein; 549 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2001; 2001WO-US031392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000; 2000US-0238557P
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV) IMMUNEX CORP.
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                                                                                                                                                                                      361 KQTSS 365
                                                                                                                                                                                                                      KQTSS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-426103/
N-PSDB; AAD37441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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27-AUG-2002
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Human, nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemia.reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

domain"

/note= "Extracellular Ig

Modified-site Modified-site Modified-site

Domain

/note= "N-glycosylated" 'note= "N-glycosylated" /note= "N-glycosylated"

'note= "N-glycosylated"

Location/Qualifiers

Modified-site

Key

Homo sapiens

/note= "Extracellular Ig domain"

.250

189.

Domain

Modified-site

domain"

/note= "Extracellular Ig

Modified-site

/note= "N-glycosylated"

.424

Domain Domain

/note= "N-glycosylated"

.342

Domain

/note= "Transmembrane domain" "C-terminal domain"

.549

/note=

WO200228902-A2

11-APR-2002

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migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above endothelial barrier function disorder which is treated by the above actimal and a stime allery, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischeroscierosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%; Score 1924.5; DB 5; Length 549; 67.9%; Pred. No. 2.8e-151; ive 33; Mismatches 62; Indels 89;
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recult pun and protein are useful for treating a disease associated with recult pun and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial created by viral polypeptide binding activity. The epithelial created by a disease associated or migration activity, wiral polypeptide binding activity. The above methoned method is inflammation, sepsis, cedema, diabetic retinopathy, astering, allograft rejection, mecastasis of cancer cells, paracallular transport disorders end as magnasis of cancer cells, paracallular transport disorders disease. Nectin DNA is also useful for the kidney or inflammatory bowel disease. Nectin DNA is also useful for thibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenesis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular sequence is human nectin-3alpha DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 89-91; 141pp; English.
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AAE23283 standard; protein; 549

Human nectin-3alpha protein

(first entry)

27-AUG-2002 AAE23283;

BXXXXXX

Youakim A;

Sorensen EA,

Lofton TE,

Baum PR, Fanslow WC,

WPI; 2002-426103/45.

(IMMV) IMMUNEX CORP

05-OCT-2001; 2001WO-US031392. 05-OCT-2000; 2000US-0238557P.

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KSVWSRLDGOWPDGLLASDNTLAFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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Matches 388; Conserv
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15-FEB-2002;
15-FEB-2002;
                                                    Friedman L,
Lioubin MN;
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                                            549;
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                                            Length
                                                                64; Indels
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                                            DB 5;
  Human nectin-3alpha gene is located on chromosome
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                                                                33; Mismatches
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10-OCT-2001; 2001US-0328605P.
22-OCT-2001; 2001US-0338733P.
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                                            70.3%;
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kidney cancer;
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                      Sequence 549
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Gaps

89;

Indels

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DB 6;

70.3%; Score 1906.5; DB 6; 67.6%; Pred. No. 9e-150; ive 33; Mismatches 64;

240

180

120 120

9 9

420

-PPPLYEERSPPLP 424

------FKQTSSIAVAGAVIGAVLALFIIA 383

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The invention relates to a novel method for identifying a candidate p53 pathway modulating agent. The method comprises providing an assay system having a purified IG polypeptide or nucleic acid, or their functionally active fragment or derivative. The method is useful for identifying modulators of the p53 pathway, particularly for identifying agents for treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung cancer or cancer of the ovary) associated with defective p53 function.

The identified modulators are useful as targets for novel therapputics. The method is also useful for diagnosing disorders associated with defective p53 function. The IG proteins or nucleic acids are useful as modifiers of the p53 pathway, and as therapeutic targets for disorders associated with defective p53 function. This sequence represents a human protein relating to the human IG genes used in the assay for identifying modulators of the p53 pathway of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a candidate p53 pathway modulators that are useful as targets for therapeutics or for diagnosing cancers associated with defective p53 function, by providing an assay system having a purified IG polypeptide
                                                                                                                                                                                                            Funke RP;
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                                                                                                                                                                                                                Francis-Lang
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2002US-0357253P.
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                                                                                                                            (EXEL-) EXELIXIS INC.
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invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This interaction destribes mover cycoscatic polymotrocitics and the properties determined were transferroun destribed in a method for diagnosing prostatic cancer. Diagnosing prostatic cancer of the requences in prostatic tissue. Screening for inhibitors of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, so bort-interfering RNA or riboxymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the aptamer against the polypeptide; and antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjected at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish percond antibody; streptavidin-conjugated horseradish percond antibody; streptavidin-conjugated horseradish eamined samples were counterstained with hemalum (blue). Malignant cells stained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
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;, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes novel cytostatic polynucleotide and
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                                                                                                                                                                                      Human prostatic carcinoma derived protein SEQ ID
                                     -----EHYDENEDDLVSHVDGSVİSRREWYV 549
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            CYODRSPGKHHONNDPKRV----YIDPREHYV
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14-MAY-2003; 2003DE-01022134
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Beckmann G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFVTVLLTPRKK--RPSYLDKVIDLPPTHK---------PPPLYEERSPPLP 424
                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTKGPDS
                                                                                                                                                                                                                                                                                                                                                                                                                         IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                                                                                                                                                                                      IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, an lymph node metastases were also stained. ADR65805-ADR66954 represent polymucleotide and polypeptide sequences used in the method of the
                                                                                                                                                                                                                                                                                             1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               89;
                                                                                                                                                                                              Length 549;
                                                                                                                                                                                                                                            64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ∄3.
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                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostatic carcinoma derived protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYQDRSPGKHHQNNDPKRV-----YIDPREHYV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; prostatic cancer;
                                                                                                                                                                                            ; Score 1906.5; DB
; Pred. No. 9e-150;
33; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EHYDENEDDLVSHVDGSVISRREWYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR66711 standard; protein; 549
                                                                                                                                                                                         70.3%;
67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2004; 2004WO-DE000433.
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                   Sequence 549 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2004
                                                                                                                                                                                                                                            Matches 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2004
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Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                                            Claim 2; Page 1205; 1607pp; German.
    27-FEB-2003; 2003DE-01009985
14-MAY-2003; 2003DE-01022134
                      DAHL E.
ROSENTHAL A.
HERMANN K.
                                                                WPI; 2004-653386/63.
                                    PILARSKY C.
                  HINZMANN B.
                                                       Xinzhong L,
                                              Hinzmann B,
                                     (PILA/)
                  (HINZ/)
                      (DAHL/)
(ROSE/)
                                                                                   agents.
                                (HERM/)
```

New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection consubstances involves a binding assay, any compounds that bind are substances involves a binding assay, any compounds that bind are predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, continerferming RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; an anti-idictype, non-human conjugated by the polypeptide against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated compostatic cancer patients, or subjects at risk, were incubated compostatic samples were counterstained with hemalum (blue). Malignant cells stained second antibody, streptavidin-conjugated horseradish concerning a second antibody; streptavidin-conjugated horseradish concerning adenocarcinoma, membrane and cytoplasmic staining was very strong, and polymetide sequences used in the method of the publicance in the paterses of the paterses of the paterses of the paterses of the paterses. invention

Sequence 549 AA;

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VLFKNYSLNDATITLENIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                                                                                                                        61 IVEPHUTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
                                                                                                                                                                              61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGF 120
                                                                                                                                                                                                                                    VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                                                                                 9
                                                                                                     1 MARTIRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLFPLLLFSRLCGALAGPI
                                                                               1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFFLLLFSRLCGALAGPI
                                         Gaps
                                         89;
70.3%; Score 1906.5; DB 8; Length 549; 67.6%; Pred. No. 9e-150; ive 33; Mismatches 64; Indels 89;
                                           Conservative
 Query Match
Best Local Similarity
                                         388;
                                                                                                                                                                                                                                      121
                       Best Loca
Matches
                                                                                                                 g
                                                                                                                                                                                                                                                             qq
                                                                                                                                                      8
                                                                                                                                                                                    g
                                                                                                                                                                                                                        8
```

LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240

181

359 360 383 | : : : | | : ::: 361 TTTLQPTIQMHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420 482 523 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 300 424 ----FKQTSSIAVAGAVIGAVLALFIIA 384 IFVIVLLIPRKK--RPSYLDKVIDLPPTHK-------PPPLYBERSPPLP 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKOPV-425 QKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQM :| : ::| | :||: | | :|| : :| | : : | | : : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : : :| : :| : : :| : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : : :| : :| : : :| : : :| : : :| : : :| : : : :| : : :| : : :| : : :| : :| : : :| : : :| : : :| : : :| : : :| : : : :| : : :| : : : :| : 183 CYQDRSPGKHHQNNDPKRV-----YIDPREHYV 510 -----EHYDENEDDLVSHVDGSVISREWYV 549 360 524 d 원 요 g à 셤 ò ò ò 8

6, 2005, 09:51:34 Search completed: October Job time: 86.2348 secs

1)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

; Search time 16.7671 Seconds (without alignments) 2926.593 Million cell updates/sec OM protein - protein search, using sw model October 6, 2005, 09:42:42 Run on:

US-09-972-268-10 2711 1 MARIPGPSFLCPGGGKAQLS......KHHQNNDPKRVYIDPREHYV 510 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	poliovirus recepto	poliovirus recepto	PRR2 delta - human		PRR2 alpha - human		poliovirus recepto	poliovirus recepto	poliovirus recepto	colon carcinoma-as	irregular chiasm C	perlecan precursor	hypothetical prote	hemicentin precurs	OX-2 membrane glyc	Down syndrome cell	adhesion molecule	surface glycoprote	neural cell adhesi	myelin-associated	myelin-associated	elastic titin - hu	myelin-associated	myelin-associated	glial cell membran	heparan sulfate pr	coxsackie- and ade	B-cell adhesion pr
SUMMARIES	ΩΙ		JC4024	A53437	I68093	HLMSP3	153960	B44194	A44194	RWHUPD	RWHUPA	A54017	A49448	A38096	T20992	T43290	A47639	T08851	JH0506	A45254	IJBONC	A61084	B33785	I38346	BNRT3S	BNRT3	A58532	S18252	JC7780	JH0371
	DB	7	N	7	N		N	~	~	1	-1	~	~	~	~	N	~	7	7	~	~ 1	-		7			~	~	~	0
	Length	407	518	530	538	467	478	392	417	392	417	416	764	4391	5175	5198	274	1896	588	588	853	626	637	7962	582	626	1091	3707	365	847
de	Query Match	43.3	20.9	19.9	19.4	17.2	16.8	15.4	15.4	14.8	14.8	12.0	8.5		7.2	•	6.9	6.7	9.9	9.9	6.5	6.5		6.5	6.5	6.5	6.4	6.4	6.3	6.1
	Score	1173.5	565.5	540	527	467	455	418	418	402	402	326.5	229.5	204.5	196.5	196.5	187.5	181.5	178	178	177.5	177	177	176	175	175	174	172.5	170.5	164.5
	Result No.	-	7	3	4	ī	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

N

RESULT JC4024

OX-2 membrane glyc	neural cell adhesi	DM-GRASP precursor	neural cell adhesi	cell adhesion mole	cell adhesion mole	cell adhesion mole	vascular cell adhe	carcinoembryonic a	neural cell adhesi	SHP substrate-1 pr	neural cell adhesi	cell surface glyco	SHP substrate-1 pr	dutt1 protein - mo	kinase-like protei
TDRTOX	IJRINC	JH0464	IJHUNG	C42632	B42632	A42632	JN0581	A36319	IJMSNG	JC5288	IJCHNL	I38049	JC5289	T30805	A39712
_	-	7	н	~	~	7	7	~	, ~ 1	7	~4	~	~	~	7
278	828	587	191	765	812	932	739	702	725	509	1091	646	513	1612	1051
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9	6.0	9	6.0	9	ý	ý	ø	Ŋ	'n.	5.	5.	'n	Ŋ	'n	ß
162.5 6.0	162.5 6.0	162 6.0	01	162 6.	162 6.	162 6.		160.5 5	160 5.		157 5.	156 5.	155 5.	154 5	153.5 5

ALIGNMENTS

RESULT 1 T08732 T08732 T08732 C; Detcial protein DKFZp566B0846.1 - human (fragment) C; Date: 11-Jun-1999 #text_change 09-Jul-2004 C; Date: 11-Jun-1999 #text_change 09-Jul-2004 C; Accession: T08732 R; Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999 A; Reference number: Z16474 A; Accession: T08732 A; Residues: 1-407 cOTT> A; Cross-references: UMIPROT: Q9Y412; EMBL:ALO50071 A; Cross-references: UMIPROT: Q9Y412; Clone DKFZp566B0846 C; Genetics: A; Note: DKFZp566B0846.1	Query Match Best Local Similarity 62.8%; Pred. No. 9.2e-79; Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;	143 SGKVICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDSLIDGGNBTVAAICIAATGKPVA 202 	203 HIDWEGDLGEMESTITSFPNETATIISOYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 262 	263 LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGGWPDGLLASDNTL 322 	323 HFVHPLTFNYSGVXICKVTNSLGQRSDQKVIYISDVP	360FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKV 403 241 EPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDYFAKN 300	404 IDLEPTH	447 NLOHSNGINSRSFDYEDENPVG 468
RESULT 1 T0873 hypothetical Cypothetical Cypothetical Cypothetical Cybote: 11-04 C;Accession: R;Ottenwaeld submitted to A;Reference 1 A;Residues: 3 A;Cosse.refen A;Crose-refen A;Crose-	Query Ma Best Loc Matches	QV Dp	ço Qo	oy op	oy qa	oy qa	oy Q	Qy

17;

65

```
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 168093
R;Eberle, F; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
R;Eberle, F; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Status: prellminary
A;Molecule type: mRNA
A;Residues: 1-530 cAOK>
A;Cross-references: UNIPROT:P32507; GB:D26107; NID:9475017; PIDN:BAA05103.1; PID:9825507
A;Experimental source: CS7/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| | :: | | : | | : | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 VEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPOSV------AVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 SFEEPILLPVTLSVRYPPEVSISGYDDNWYLGRSEAILTCDVRSNPEPTDYDWSTTSGVF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 PSQLFTLGASEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGPLLLGATGLGPSLLV 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 PASAVAQGSQL-LVHSVDRMVNTTFICTATNAVGTGRAEQVILVRESP--STAGAGATGG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 LLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VLPPSRLSPTLPLLPLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KEREVGNLQHSNGLN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SRSFDYEDENPVGEDGIQQMYPLYNQMCYQDRSPGKHHQNND 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%; Score 540; DB 2; 28.8%; Pred. No. 5.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.4%; Score 527; DB 2;
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-538 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQK--DLFQPEHLPLQTQF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 153; Conservative
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C.Superfamily: poliovirus receptor; immunoglobulin homology
C.Superfamily: poliovirus receptor; renamembrane protein
C.Superfamily: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-318/Product: poliovirus receptor-related protein #status predicted <MAT>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;35-379/Domain: transmembrane #status predicted <IRMN>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A53437

A53437

Coliovirus receptor mPVR - mouse

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A53437

C;Accession: A53437

C;Accession: A53437

B;Aoki, J, T; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.

J. Biol. Chem. 269, 8431-8438, 1994

A;Title: Amino acid residues on human poliovirus receptor involved in interaction with
    poliovirus receptor-related protein precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: J-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; I Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human g A;Reference number: JC4024; MUID:95237621; PMID:7721102
A;Ression: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 aLOD>
A;Cross-references: EMBL:X76400; NID:9732795; PIDN:CAA53980.1; PID:9732796
A;Genetics: A;Gene: GDB:PRNA
A;Cross-references: A;Gene: GDB:PRNA
A;Cross-references: A;Gene: GDB:PRNA
A;Cross-references: A;Gene: GDB:PRNA
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A;Cros
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SYEEEEEEEEGGGGGERKVGGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YISDVPFKQTS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLD 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.9%; Score 565.5; DB 2; Length 518; 29.0%; Pred. No. 7.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 KKHVYGNGYSKAGIPQHH--PPMAQNLQYPDDSDD-
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455

423

Best Local Similarity 27.3%; Pred. No. 5.4e-31; Matches 151; Conservative 94; Mismatches 206; Indels 102; Gaps 21;	
QY 33 PPTPPPLLLLEPPLLESRL-CGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQ 88	Qy 30 ILQPPTPPPLILLIFPLILFSRLCGALAGPIIVBPHVTAVWGKNVSLKCLIEVNETIT 87 :
89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGSYQG-RVLFKNYSLNDATITL:	OY 88 QISWBKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDATITLHNIG 139
136 HNIGESDSGKYICKAVTEPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET : : : :	Qy 140 FSDSGKYICKAVTFPLGNAQSSTTVIVLVEPTVSLIKGFDSLIDGGNETVAAICI 194
128 HGLTVEDEGNYTCEFAIFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDPT 189 VAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETAIISQYKLFPTRFARGR	QY 195 AATGKPVAHIDWEGDLGEMESTITSFPNBTAIIISQYKLFPTRFARGRRITCVVKHP 251 176 STGGRPPARITWISSLGG-EAKDIQEFGIQAGTVIIISRYSLVPVGRADGVKVTCRVEHB 234
DD 179 TYCKVERPERISYMEAKETUVSTIDMEAKETUVSGILAG1717ISKFTLVFSGKADGV 234 QY 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFKS 302	QY 252 ALEKDIRYSFILDIQYAPEVSYTGYDGWWFVGRKGVNLKCNADANPPPFKSVWSRLDGGW 311 :
	Qy 312 PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAV 368 Db 295 PASAVAQGSQL-LVHSVDRMVNTTFICTATNAVGTGRAEQVILVRDTPQASRDVGPLV 351
363 TSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPP-P :	QY 369 AGAVIGAVIALFITAIFVT-VLITPRKKRPS 398
QY 415 LYEERSPPLPQKDLFQPEHLPLQTQFKERREVGNLQHSNG 453	RESULT 6 153960 PRR2 alpha - human
454LNSRSFDXED-ENPVGEDGIQQMYPLYNQMCYQDRSPGRHQNND	
498 PKKYIDPREHY 510	Gene 159, 267-272, 1995 A.Pitle: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the Reference number: 15,960: MUID: 93,3476,10: PMLD: 7622062
Db 528KGFVMSRAMÝV 538 RESULT 5	A,Accession: 153960 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Rolecule type: mRNA A,Residues: 1-478 <res></res>
HLMSP3 poliovirus receptor homolog precursor - mouse C;Species: Mus musculus domesticus (western European house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: A3821	A,Cross-references: UNIPROT:Q9UEI6; GB:S79171; NID:g1042202; FID:g1042203 C;Genetics: A;Gene: PRRSalpha A;Gene: PRRSalpha C;Superfamily: poliovirus receptor; immunoglobulin homology F;276-331/Domain: immunoglobulin homology <imm></imm>
R;Morrison, M.E.; Racaniello, V.R. J. Virol. 66, 2807-2813, 1992 A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus re A;Reference number: A38211; MUID:92219365; PMID:1560525	Query Match 16.8%; Score 455; DB 2; Length 478; Best Local Similarity 30.3%; Pred. No. 9.38-26; Matches 121; Conservative 67; Mismatches 159; Indels 52; Gaps 13;
A.Accession: A38211 A.Molecule type: DNA A.Residues: 1-467 <mor> A.Cross-references: INTOPROT.P22507: GR-WR0206: NID:c199785: PIDN:AAA39734.1: PID:c199786</mor>	Qy 33 PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQ 88
s receptor; immunoglobulin homology glycoprotein; transmembrane protein quence #status predicted <sig></sig>	89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGSYQG-RVLFKNYSLNDATITL
;26-354/Domain: extracellular #status predicted <ext>;47-133/Domain: immunoglobulin homology <imm1>;167-21/Domain: immunoglobulin homology <imm2>;227/Domain: immunoglobulin homology <imm3></imm3></imm2></imm1></ext>	136 HNIGESDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET
F;355-374/Domain: transmembrane #status predicted <tmn> F;375-467/Domain: intracellular #status predicted <tmt> F;575-467/Domain: intracellular #status predicted F;54-131,174-229,274-320/Disulfide bonds: #status predicted F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmt></tmn>	QY 189 VAJICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR 242
Query Match 17.2%; Score 467; DB 1; Length 467; Best Local Similarity 32.5%; Pred. No. 1.2e-26;	QY 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302

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A,Molecule type: mRNA A,Residues: 1-66,74,68-392 «MEN> A,Residues: 1-66,74,68-392 «MEN> A,Gross-references: GB:MJ4406 C,Comment: The normal function of this receptor is unknown. Membrane-bound and soluble fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Antrones: 27/1, 1445/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane prof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.; Take
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A,Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A,Reference number: A90910; MUID:89168426; PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A43024; B31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Ilzuka, N.; Takeuchi, R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Ilzuka, N.; Takeuchi, A;Title: The poliovirus receptor protein is produced both as membrane-bound and A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                     91 WEKIHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 TVYYPPEVSISGYDNNWYLSQNEATLICDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGOWPDGLLASDNTLH 323
                                                                                                                                                                                                                                                                                       90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 PPLLLLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQIS
                                                                                                                                                                                                                                                                                                                  PPLILILIEL----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 WEGDLGEMESTTTS--FPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 FVHPLIFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALF
                                                                                                                                                                                                                                          28;
                                                                                                                                                                                           Length 417;
                                                                                                                                                                                         15.4%; Score 418; DB 2; Length 41 30.6%; Pred. No. 4.1e-23; ive 64; Mismatches 162; Indels
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.417 ckOl>
A;Cross-references: UNIPROT:P32506; GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poliovirus receptor splice form delta precursor
N'Alternate names: poliovirus receptor H20B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P15151; EMBL:X64116
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
                                                                                                                                                                                         Query Match
Best Local Similarity 30.69
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 IIAIFV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-392 <KOI>
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94.194

901 ovitus receptor (clone AGW-alpha-1) - green monkey

C.Species: Cercopithecus aethiops (green monkey, grivet)

C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C.Accession: A44194

B.Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A.Fitles: A second gene for the African green monkey poliovirus receptor that has no puta

A.Reference number: A44194; WUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                               puta
                                                                                                                                                                                                                                                                                                           poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Accession: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no jakeference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEGDLGEMESTITS -- FPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQWPDGLLASDNTLH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 FVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDVRSNPEPTGY 294
                                                   VWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF-K 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLILITLEL----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMETHVSQLT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFEKPQLLTVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEKIHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NET-ITOIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.4%; Score 410; DB 2; Length 39 Best Local Similarity 30.6%; Pred. No. 3.8e-23; Matches 112; Conservative 64; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P12506; GB:848817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                               362 QTSSIAVAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
                                                                                                                                                                             IIAIFV 386
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LLGIGV 363
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C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane proc
F;1-20/Domain: signal sequence #status predicted <576>
F;21-41/Product: poliovirus receptor alpha #status predicted <PVRA>
F;21-343/Domain: extracellular #status predicted <EXTP
F;21-343/Domain: extracellular #status predicted <EXTP
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Domain: immunoglobulin homology <IMM1>
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1. Biol. Chem. 269, 15601-15605, 1994
A; Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinom.
A; Reference number: A54017; MUID:94253144; PMID:8195207
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AjTitle: Characterization, isolation and amino terminal sequencing of a rat colon carcinc A,Reference number: A61206; MUID:91184910; PMID:2010233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLGGMPNTSQVPGFLSGTVTVTSLWILLVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLIFNYSGVYICKVINSLGQRSDQKVIYISDVPFKQTSSIAVAGAVIGAVLALFIIAIFV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
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C;Accession: A54017; A61206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;349-367/Domain: transmembrane #status predicted <TMN>
F;368-417/Domain: intracellular #status predicted <IMT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Mismatches 163; Indels
                                                            A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
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                       GDB:120324; OMIM:173850
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C,Species: Rattus norvegicus (Norway rat)
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A, Residues: 34-41,'X', 43-53 <CH2>
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Best Local Similarity
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-392/Product: poliovirus receptor delta #status predicted <MAT>
F;21-34/Domain: extracellular #status predicted <EXT>
F;21-34/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM2>
F;359-314/Domain: immunoglobulin homology <IMM3>
F;344-36/Domain: transmembrane #status predicted <ITM>
F;368-392/Domain: intracellular #status predicted <ITM>
F;368-392/Domain: intracellular #status predicted <ITM>
F;368-312/Domain: intracellular #status predicted <ITM
F;368-312/Domain: intracellular #status predicted <IT
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A; Residues: 1-417 <KOI>
A; Residues: 1-417 <KOI>
A; Cross-references: UNIPROT: PISIS1; UNIPROT: Q96BJ1; EMBL: X64116; NID: g35809; PIDN: CAA454
A; Note: 67-Ala was also found
A; Note: the gamma form has 331-Gly and lacks residues 332-384
B; Mendelsohn, C.L.; Wimmer, B.; Racaniello, V.R.
Cell 56, 855-865, 1989
A; Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A; Reference number: A90910; MUID: 89168426; PMID: 2538245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 PVDKPINTTLICNVTNALGAROAELTVOVKEGPPSEHSGMS-RNAIIFLVFLILL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 WPLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Score 402; DB 1; Length 39. 29.3%; Pred. No. 5.7e-22; ive 67; Mismatches 163; Indels
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Best Local Similarity 29.39
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NyAlternate names: irreC-roughest protein
NyAlternate names: irreC-roughest protein
NyAlternate names: irreC-roughest protein
NyAlternate names: irreC-roughest protein
CyBecises Drosophila melanogaster
CyBecises Drosophila melanogaster
CyBecises Drosophila melanogaster
CyAccession: A4948; S34129
CyRamos, Tiglol, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst
Genes Dev. 7, 2533-2547, 1993
Ayreference number: A4948; MUID:94102535; PMID:7503814
AyReference number: A4948; MUID:94102535; PMID:7503814
Ayreference number: A4948
Ayreference NA; mRNA
Ayreferences: DNA; mRNA
Ayreferences: UNIPROT:Q08180; GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NI
                      cel
A,Note: the residue at position 9 is suggested to be glycosylated asparagine
C,Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma
C,Keywords: glycoprotein; membrane protein
                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- DDFGLGTSRDLSG---FERYAMVGSDEEGDYSLDIYPVMLDDD 102
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                                                                                                                                                                                                                                                                                                                                                      105 VYEDLRNASLAISNIRVEDEGIYECQIATFPTGSKSANVWLKVFARPKNTAEALEPSPTL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                               165 MPQD----VAKCISADGHPPGRITWSSNVNGSYREMKETGSSRAPPQLSATSPWCLLARQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSG-VYICKVTNSLGQRSDQKVIYIS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVWGKNVSLKCLI--EVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF-K 124
                                                                                                                                                                                                                                                                                 45 GFLGGSTVLHCSLASKDNVTITQLTWMKRDPDGSPFRACLPPQEGPSISDPERVKFLVAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
                                                                                                                                                                                                                                                                                                                           NY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSL 181
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                                                                                                                                                                                       2 APLA-GASRSRVWSAGL------LRLLLLSCFTLQKAGGEIA--VQVLSNST
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                                                                                                                                                                8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVT
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; Pred. No. 7e-09;
65; Mismatches 153;
                                                                               12.0%; Score 326.5; DB 2; 28.1%; Pred. No. 2.2e-16; ive 56; Mismatches 171;
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A;Gene: FlyBase:rst
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein
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95; Conservative
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                                                                                                    Similarity
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perlecan precursor - human
N/Alternate names: basement membrane heparan sulfate protecglycan; heparan sulfate protec
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Cipacies: Homo sapiens (man)
Cipacies: On-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
Cipacession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
RiMurdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A; Title: Primary structure of the human heparan sulfate proteoglycan from basement membritor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A; Reference number: A38096; MUID:92235084; PMID:1569102
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J. Cell Biol. 116, 559-571, 1992
J.Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD prolel adheaton molecules, and epidermal growth factor.
A;Reference number: A41736; MUID:92112994; PMID:1730768
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A; Residues: 1-57, 'D', 59-434,'A', 436,'FL', 438-449,'Q', 451-502,'A', 503-792,'K', 794-908,'R',
71-2919,'H', 2081-2994,'G', 2996-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-318,'C.
71-2919,'H', 2081-2094,'G', 2996-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-318,'R', 31629-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-418,'R', 31639-394,'G', 2996-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-418,'R', 31639-396,'R', 3163
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A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclona
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A;Cross-references: UNIPROT:P98160; GB:M85289; NID:G184426; PIDN:AAA52700.1; PID:G184427
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A; Readdudes: YTT, 492-908, RR', 910-1101, LL', 1103-1132, LL', 1134-1221, 'L', 1223-1397 < KA2>
A; Readdudes: YTT, 492-908, RR', 910-1101, 'L', 1103-1132, LL'; PID: 9243371
A; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzc
Genomics 10, 673-680, 1991
A; Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cell:
A; Reference number: A40306; WUID: 91365376; PMID: 1679749
                                                                                                                                                                                                                                                               289
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---EMESTTTSFPNETA-TIISQYKLFPTRFARGRRITCVVKHPALE 254
                                                                                                                               163 AAEITWIDGLGNVLTDNIEYTVIPLPDQRRFTAKSVLRLTPKKEHHNTNFSCQAQNTA-D 221
                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1018-1405, G', 1407-1409, 'G', 1411-1465 < DOD>
A; Cross-references: GB: M64283; ND: g184424; PIDN: AAA52699.1; PID: g184425
K; Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J. Cell Biol. 109, 3199-3211, 1989
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A;Reference number: A33625; MUID:90078352; PMID:2687294
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A, Accession: T43290
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A; Residues: 1-5175 <WI2>
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88; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 -- PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLCPGGGKAQLS-SASLLGAGLL--LOPPTPPPLLLLLFPLLLFSRLCGALAGPIIVE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%; Score 204.5; DB 2; Length Best Local Similarity 24.1%; Pred. No. 5.1e-06; Matches 89; Conservative 58; Mismatches 150; Indels
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Accession: B33625
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A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
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C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43290; T2093; T24734
R;VOGE1, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
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A;Experimental source: clone T09B9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      892 VPPEEQLIEGQDLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLL 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF 234
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: 720992; T24733
Submitted to the EMBL Data Library, December 1994
A;Seference number: Z19355
A;Accession: T20992
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: UNIPROT:076518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
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A;Acceptor number: 219929
A;Acceptor: 724733
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hypothetical protein F15G9.4a - Caenorhabditis elegans

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submitted to the EMBL Data Library, December 1994

A;Reference number: 219355

A;Accession: T20993

A;Accession: T20993

A;Accession: Preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-5198 «WIL>
A;Cross-references: EMBL:247068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:FI5G9.4b

A;Residues: 21992

A;Reference number: 21992

B;Reference number: 21992

A;Accession: T24734

A;Reference number: 21992

A;Accession: T24734

A;Residues: 1-5198 «WIL>
A;Reference number: 21992

A;Accession: T24734

A;Residues: 1-5198 «WIL>
A;Residues: 1-5198 «WIL>
A;Residues: 1-5198 «WIL>
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Matches 88; Conservative
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Search completed: October 6, 2005, 10:21:09 Job time: 17.7671 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database

	Description	Q9jlb8 mus musculu	Q9jlb7 mus musculu	Q9ngs3 homo sapien	Q6nvz3 homo sapien	พนธ ก	Q9d006 mus musculu	homo	homo	рошо	Q9jkf6 mus musculu	Q6p9m9 mus musculu		Q15223 homo sapien	P32507 mus musculu	Q80xj5 mus musculu	_	Q9g174 cercopithec	Q92692 homo sapien	Q9g175 bos taurus	Q96ny8 homo sapien	Q96k15 homo sapien	Ogdbp8 mus musculu		Q8ced8 mus musculu	Q8r007 mus musculu	Q66j72 xenopus lae	Q8c6f2 mus musculu	Q91vt9 mus musculu	Q9uei6 homo sapien		Q9r1el rattus norv
SUMMARIES	ΠD	Q9JLB8	Q9JLB7	O9NQS3	Q6NVZ3	Q9JLB9	Ф3D006	QBNC05	Q9Y412	Q9BVA9	PVR1 MOUSE	Q6P9 <u>M</u> 9		PVR1_HUMAN	PVR2_MOUSE	Q80X J 5	Q9ERF5	Q9GL74	PVR2 HUMAN	_	_		_		_	Q8R007	_		_		PVR_CERAE	Q9RIE1
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181 LIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240

Q8hy16 cebus apell Q65611 rattus norv P15151 homo sapien Q91wpl mus musculu Q8kO94 m hypotheti Q8By16 mus musculu Q8By15 lemur catta Q8hy15 lemur catta Q8hy14 oryctolagus Q60977 mus musculu Q7m048 rattus norv Q7tn11 mus musculu Q9by67 homo sapien Q66kx2 xenopus lae		odate) update)	ebrata; Euteleostomi; Muridae; Murinae; Mus.	4/jbc.275.14.10291; , Miyahara M., e cell adhesion molecules ell adhesion	; IDA.	54 CRC64;	2; Length 510; 73; 31; Indels 2; Gaps 2;	MARTPGPSPI.CPGGGKAQLSSASLLGAGLLQPPTPPPLLLLIFPILLFSRLCGALAGPI 60 	VEPHVTAVWGKOVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120 	FKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 	LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPPTRFAR 240
Q8HY16 Q63611 Q918HUMAN Q91WP1 Q8RO94 Q8BNY6 Q8BNY6 Q8HY14 Q60977 Q7MQ48 Q7TNL1	ALIGNMENTS PRT: 510 AA	Created) Last sequence up	ta; Craniata; Verte	5 : X O	activities; J. Biol. Chem. 275:10291-10299(2000). EMBL; AF195834; AAF63686.1; MGD; MG1:1930171; Pvrl3. GO; GO:0005913; C:cell-cell adherens junction. GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0005515; P:profein hinding: TAS.	.1 adhesion; IDA. ke. 3. 45CFEGEF7845486	; Score 2406; DB 2 ; Pred. No. 9.9e-17: 22; Mismatches 3	OLSSASLLGAGLLLQPPTP CLSSAFPPAAGLLLPAPTP	CLIEVNETITQISWEKIHG: 	IGFSDSGKYICKAVTFPLG IGFSDSGKYICKAVTFPLG	GKPVAHIDWEGDLGEMEST
155.0 144.9 14	PRELIMINARY:	(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 26,	(Mouse). (Mouse). (Mouse). (Mouse). (Mosoutheria; Modentie (Mosoutheria)	M N.A. 9403; PubMed=1 wa K., Nakanis , Mizoguchi A. new member of	; m. 275:10291-1 34; AAF63686.1 0171; Pvrl3. 13; C:cell-cel 15; C:extracel 21; C:integral 15: F:protein	(6337, P:Cell-Cell IPR003599; IG. IPR007110; IG-li 0047; IG; 1. 00409; IG; 1. 550835; IG LIKE;	88.7% Similarity 89.2% 6; Conservative	TPGPSPLCPGGGKA TPGPAPLCPGGGKA	PHVTAVWGKNVSLK PHVTAVWGKNVSLK	KNYSLNDATITLHN KNYSLNDATITLHN	GGNETVAAICIAAT
32 407 33 406.5 34 406.5 35 400.5 37 399.5 39 390 40 386 41 355.5 42 300.5 44 305.5 45 304.5	SULT 1 JLB8 D94ILB8	Q9JLB8; 01-OCT-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel. 01-OCT-2004 (TrEMBLrel.	Muse=Pvrl3; Mus musculus (Mouse Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;	L1) SEQUENCE FRO MEDLINE=2020 Satch-Horika Tachibana K. "Nectin-3: a that shows h	ACLIVICIES." J. Biol. Che EMBL, AF1958 MGD, MGI:193 GO, GO:00056 GO, GO:00160 GO: GO:00160	GO, GO: 00163 InterPro; IP InterPro; IP Fram; PF0004 SMART; SM004 PROSITE; PSS SEQUENCE 5	Query Match Best Local Simi Matches 456;	1 MAR 1 MAR	61 IVE 61 IVE	121 VLF 121 VLF	181 LID
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121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
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                                 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                              241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-like.
Pfam; PF00047; ig; 1.
SWART; SW00409; IG; 1.
SWART; PS00835; IG LIKE; 3.
SEQUENCE 549 AA; G1002 MW; 6D1104CCB4A9D731 CRC64;
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                                                                                                                                                             KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYBERS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291; Satch-Horikawa K., Nakanishi H., Takahashi K., Miyahara M., Tachibana K., Mizoguchi A., Takahashi K., Miyahara M., "Nacouchi A., Takahashi K., a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                                    GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
   LIDGGNETVAAVCVAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTRFAR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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SMO0409; IG; 1.
E; PSSO835; IG LIKE; 3.
2A0A4416E5B02FEF CRC64; ... 7. 1.engt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activities.",
J. Biol. Chem. 275:10291-10299(2000).

MRBL; AF195815; AF63687.1; -.

MGD; MG1:1930171; Pvrl3.

GO; GO:0005913; C:cell-cell adherens junction; IDA.

GO; GO:00165015; C:extracellular space; TAS.

GO; GO:0016501; C:integral to membrane; TAS.

GO; GO:0015015; F:protean binding; IPI.

GO; GO:0015337; P:cell-cell adhesion; IDA.
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InterPro; IPR007110; Ig-11ke.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 3.
REDIENCE 549 AA; 60582 MW;
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Matches 371; Conservative
                         Matches 353; Conservative
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschul S.F., Zeeberg B., Buetow K.A., Rubin G.M., Hong L.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soarse M.B., Bonaldon M.F., Carannori P.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malek J.A., Gunzatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                             ----FKQTSSIAVAGAVIGAVLALFIIA 383
                                                                                                                                                                                                                                                                                                                 425 QKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQM 482
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                            479 -NNLIRKDYLEEPEKTOW-----NNVENLNRF-ERPMDYYEDLKMGMKFVSD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; AF195833; AAF65685.1; -.
MGD; MG1:13930171; Pvrf3.

GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005515; F:procein binding; IPI.
GO; GO:001637; P:cell-cell adhesion; IDA.
InterPro; IPR003999; IG.
InterPro; IPR007110; I9-like.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cell adhesion molecule nectin-3 alpha.
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01.MR-2004 (TrEMBLrel. 26, Last annotation update)
MOS musculus 10 days embryo whole body CDNA, RIKEN full-length
enriched library, clone:2610301B19 product:poliovirus receptor-related
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STRAIN=CS7BL/6J; TISSUB=Whole body;
STRAIN=C927927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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STRARIESSEL/G1; TISSUE=Whole body;
MEDILNE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSOCTAIUM;
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STRAIN=CS7BL/6J; TISSUE=Whole body;
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EMBL, AKO11949; BAB27933.1; ...

ROG GO:0005513; C:etl-cellular space; TAS.

GO; GO:001621; C:integral to membrane; TAS.

GO; GO:001621; C:integral to membrane; TAS.

GO; GO:001631; F:protein binding; IPI.
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SEQUENCE FROM N.A.
STRAIR-278L/GD, TISSUE-Whole body;
STRAIR-278L/GD, TISSUE-Whole body;
MEDLINE-2078L/GD, TISSUE-Whole body;
MEDLINE-2078L/GD, TISSUE-WHOLE BODI-10.1101/gr.145100;
Cardinoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=257BL/63; TISSUE=Whole body;
MEDLINE=26350913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishin K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
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ive 38; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 10:1757-1771(2000).
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InterPro; IPR007110; Ig-like.
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Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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:||: :|| | : :| | | | 301 Y-IPPSDMQKESQIDVLQQDELDPYPDSVKKENKNPVNNLIRKDYLEFPEKTQW-----N 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HFVHPLTFNYSGVYICKVINSLGQRSDQRVIYISDPPTTTTLQPTIQWHPSTADIEDLAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 SGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 HIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI
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   SFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AlOS0071; CAB43256.1; -...
PIR; T08732; T08732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%; Score 1173.5; DB 2; Length 407; 62.8%; Pred. No. 5.8e-80; ive 28; Mismatches 51; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;
                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp566B0846 (Fragment).
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Last sequence update)
Last annotation update)
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355 NVENLNRF-ERPMDYYEDLKMG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 2.
Hypothetical protein.
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(TrEMBLrel. 17, L
(TrEMBLrel. 25, I
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Best Local Similarity 62.89
Matches 240; Conservative
                                                               279 NWFVGRKGVNLK 290
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                                                                                                           NWFVGGKGVNLK
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SEQUENCE FROM N.A.
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01-JUN-2001 (
01-OCT-2003 (
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GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                 KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQKVIYISDPPT 360
                                                                                                                                                                                                                                                                                                     | ::: | | ::: | | ::: | 361 TTTLQPTVQWHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGGALFLVLVS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSSTTVTVLVBPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 195
                                                                                                                                                                                                                                                            361 KQT-----VAGAVIGAVLALFIIA 383
                                                                                                                                                                                                                                                                                                                                                                                            384 IFVTVLLTPRKKR------PSYLDKVIDLPPTHK-----PPPLYEERSPPLPQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 ILAGVFCYRRRRFFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYPDSVKKENKNPV-- 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 LLRGPLLPRSFSGNPRALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
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                                                                                                                               KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 KDLFQPEHL--PLOTQFKEREVGNLQHSNGLNSRSFDYEDENPVG------EDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLFPLL--LFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanaqi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR003199; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypotherical protein FLJ90624.
Hypotherical protein FLJ90624.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 2.
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Best Local Similarity 96.0°
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TISSUE=Placenta;
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262 120 322 180

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Best Local Sim
Matches 154;
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                         61 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQ 120
                                                                                                                                                                                                                                                                                                                                                           121 PTIQWHPSTADIEDLATEPKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGI 180
                                                                                                                                                                                                                                                                                           RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP---- 359
                                                                                                                                                                                                                                                                                                                                          ------FKOTSSIAVAGAVLALFIIAIFVTV 388
                                                                                                                                                                                                                                                                                                                                                                                          389 LLTPRKK--RPSYLDKVIDLPPTHK-------PPPLYEERSPPLPQKDLF 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 RKDYLEEPEKTOW----NNVENLNRF-ERPMDYYEDLKMGMKFVSD------- 278
                                                                                                                                                                                                                                                                                                                                                                                                                181 FCYRRRRTFRGDYFAKNY-IPPSDMOKESQIDVLQQDELDSYPDSVKKENKNPV--NNLI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                         QPEHL---PLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQMCYQDR 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867; Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.; The murine homolog of human nectini delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD."; Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                                                                                                                                                                                       246 CVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFKSVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVRI MOUSE STANDARD; PRT; 515 AA.

Q9JKF6; Q9ERL5; Q9J117;
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).

Name=Pvrl1; Synonyms=HveC, Prrl;
          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                    89;
                                                                                                                                                                                            23.9%; Score 648.5; DB 2; Length 304;
                                                                                                                                                                                                                    62; Indels
                                                                               TISSUE=Cervix;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;
to nectin 3; DKFZP566B0846 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20541977, PubMed=11090177;
DOJ=-10128/JV1.74.24.11773-11781.2000;
Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
                                                                                                                                                                                                      Pred. No. 1.5e-40;
                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EHYDENEDDLVSHVDGSVISREWYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPGKHHQNNDPKRV----YIDPREHYV
                                                                                                                  EMBL, BC001336, AAH01336.1; -
InterPro; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                         44.18;
                                                                                                                                                                                                                    Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                         Best Local Similarity
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                                                                     SEQUENCE FROM N.A.
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                                              NCBI_TaxID=9606;
                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                           306
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Extracellular (Potential).

Cytoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Poly-Glu.

Poly-Glu.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%; Score 602; DB 1; Length 515;
ilarity 30.4%; Pred. No. 9.5e-37;
Conservative 90; Mismatches 162; Indels 100; Gaps
                                                                                                                                                                                                           Zhan J., Wimmer E.; "MPRRI), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural
"Striking similarity of murine nectin-lalpha to human nectin-lal; (HveC) in sequence and activity as a glycoprotein D receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L -> P (in Ref. 1).
N -> D (in Ref. 1).
P -> PP (in Ref. 2).
S -> G (in Ref. 3).
FFFGOREBSFFB7A0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1926483; Pvrll.
GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; IDA.
InterPro; IPR007110; Ig-like.
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                                                                                     Virol. 74:11773-11781(2000)
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57064 MW;
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                                                                                                                                                                                     STRAIN-Swiss Webster;
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515 AA;
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Altasuberg R.L., Feingold E.A., Groues L.H., Darged J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunbaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhety J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Green Eatlon and initial analysis of more than 15,000 full-length human
                                                                                                                                                                             223 SLACIVNY-HLDR-FRESLTLINVQYEPEVTIEGFDGNWYLQRIDVKLICKADANPPATEY 280
                                                                                                                                                                                                                                                                                                                                                  303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
                                                                                                                                                                                                                                                                                                                                                                            433 SSYEEEEEEGGGGGERKVGGPHPKYDEDAKRPYFTVDEAEARODGYGDRILGYOY---D 489
GTDVVLHCSFANPLPSVKITQVTWQKASNGSKQNMAIYNPTMGVSVLPPYEKRVEFLRPS 103
                                                                                                                                                                                                                                                 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSS-----IAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPP 413
                                                                            104 FIDGTIRLSGLELEDEGMYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG
                                               LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                             -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLYEERSPPLPQKDLFQ-----SNGLNS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 HWTTLNGSLPKGVEAONRTLFFRGPITYSLAGTYICEATNPIGTRSGOVEVNITEFPYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 FIDGTIRLSGLELEDEGGYYLCEFATFPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 KAGIPOHH--PPMAQNLQYPDDSDD------EKKAGPLGGS----SYEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Neclin 1).
Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match . 22.1%; Score 598; DB 2; Length 51
Best Local Similarity 31.0%; Pred. No. 1.9e-36;
Matches 155; Conservative 86; Mismatches 171; Indels
(NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;
                SUMBLY BOOOS 10. The Embly Genealty Date and Sumblified (NOV-2003) to the Embly Genealty Date of GO; GO: 6005513; C: cell-cell adherens junction; IDP GO; GO: 6005513; C: cettracellular space; TAS. GO; GO: 6005515; C: integral to membrane; TAS. GO; GO: 6005515; F: protein binding; IPI. GO; GO: 600482; F: preceptor activity; IDA. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. C. InterPro; IPR003596; Ig. V. Pfam; P00047; ig; 1. SMART; SM00409; IG; 2. SMART; SM00409; IG; 2. SMART; SM00409; IG; 2. SMART; SM00406; IGV; 1. PROSITE; PS50835; IG_LIKE; 2.
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Q9GL76;
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LGORSDOKVIYISDVPFKQTS-----SIAVAGAVIGAV-LALFIIAIFVTVLLTP 392
                                                           TATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVG 283
                                                                                             TVTVISRYRLVPSREDHROSLACIVNYHM - DRFRESLTLNVQYEPEVTIEGFDGNWYLQ 261
                                                                                                                                    RKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS 343
                                                                                                                                                                                                                                   ----E 425
                                                                                                                                                                                                                                                                                                                                                                  --- QMCYQD 486
                                                                                                                                                                                                                                                                                                                                                                                                    KKAGPL----GGSSYEBEBEBEGGGGERKVGGPHPKYDEDAKRPYFTVDEABARQDGYGD 481
                                                                                                                                                                                                                                                                                       RKK-RPSYLDK------VIDLPPTHKPPPLYBERSPPLPQKDLFQPEHLPLQTQFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cDNA characterization and chromosomal localization of a gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
MEDLINE=20392396; PubMed=10932188; DOI=10.1038/78119;
Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Entry of alphaherpesviruses mediated by poliovirus receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-98279152; PubMed-9616127; DOI=10.1126/science.280.5369.1618;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-2527621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    simplex virus (HSV) recep positively and negatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            015273; 075465; Q9HBE6; Q9HBW2;
16-OCT-2001 [Rel. 40, Created)
16-OCT-2001 [Rel. 40, Last sequence update)
05-UUL-2004 [Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM GAMMA).
MEDLINE=21256041; PubMed=11356977;
DOI=10.1128/JVI.75.12.5684-5691.2001;
Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
Campadelli-Fjume G., Dubreuil P.;
"Novel, soluble isoform of the herpes simplex virus (HSV) renectin1 (or prr1-HigR-Hvec) modulates positively and negativ
                                                                                                                                                                                                                                                                                                                                                                  REVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYN-----
                                                                                                                                                                                                                                                                                                                            RHTFKGDYSTKKHVYGNGYSKAGIPQHH--PPMAQNLQYPEDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515
                                                                                                                                                                                                                                                                                                                                                                                                                                             487 RSPGKHHQNNDPKRV------YIDPREHYV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTLGYQY --- DPEQLDLAENMVSQNDGSFISKKEWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 1 and poliovirus receptor.";
Science 280:1618-1620(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       susceptibility to hav infection."; J. Virol. 75:5684-5691 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the poliovirus receptor gene.";
Gene 155:261-265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM DELTA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CD111 antigen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVR1 HUMAN
                                                                                               204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCGALAGPIIVEPHVTAVWGKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 MGVSVLAPÝRERVEFLRPSFTDGTÍRLSRLELEĎEGVÝÍČEFATFPAGNRESQLNLTVMA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 EPTVSLIKGPDSLIDG----GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGAHTQVVQVNDSMYGFIGTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPA 84
                                                                                                                                                                                                                                                     alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                      "Porcine HveC, a member of the highly conserved HveC/nectin 1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity) SUBCELLULAR LOCATION: TYPE I membrane protein. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poliovirus receptor related protein 1. Extracellular (Potential).
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(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                 unordata; Craniata; Vertebrata; Buteleostomi;
Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                        is a functional alphaherpesvirus receptor.";
Virology 281:315-328(2001).
-!- FUNCTION: Probably involved in cell adhesion. Receptor for
                                                                                                                  MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
                                                                                                                          Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
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Ig-like C2-type 1.
Ta-like C2-type 2.
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9.1e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
Cell adhesion; Glycoprotein; Im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF308632; AAG30281.1; -. HSSP; Q05793; 1GL4.
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SIGNAL 1
                                         Mammalia; Eutheria;
 Sus scrofa (Pig).
Eukaryota; Metazoa;
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515 AA;
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156; Conserv
                                                                                             SEQUENCE FROM N.A.
                                                           NCBI_TaxID=9823;
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                                                                                                                                                                                                                                             Name=Gamma;
Isold=015223-3; Sequence=VSP 002624, VSP 002625;
Isold=015223-3; Sequence=VSP 002624, VSP 002625;
Isold=015233-3; Sequence=VSP 002624, VSP 002625;
DISSASS: Defects in PVRL1 are a cause of cleft lip/palate-
ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
responsible for allelic forms known as Margarita island ectodermal
dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
                                                                                                               SUBGINIT: Interacts with HSV glycoprotein D (gD).
SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                         for
entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO:0005912; C:adherens junction; NAS.
R GO; GO:0016021; C:adherens junction; NAS.
R GO; GO:0016021; C:integral to membrane; NAS.
R GO; GO:0016021; P:cell-cell adhesion; NAS.
R GO; GO:0016337; P:cell-cell adhesion; NAS.
R GO; GO:0046718; P:viral entry; NAS.
R GO; GO:0046718; P:viral entry; NAS.
R HorePro; IPR00110; Ig-1ike.
R InterPro; IPR003596; Ig_v.
R Ffam; PP00047; Ig; 2.
R RART; SM00406; IGv; 1.
R PROSITE; PS50935; IG_LIKE; 2.
R PROSITE; PS50935; IG_LIKE; 2.
R Alternative splicing; Cell adhesion; Glycoprotein;
R Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.
T SIGNAL
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               cell-cell adhesion
in cleft lip/palate-ectodermal
Helms J.A., Spritz R.A.;
whtataions of PVRL1, encoding a cell-cell adhesion
molecule/herpesvirus receptor, in cleft lip/palate-ectoderm
dysplasia..;
Nat. Genet. 25:427-430(2000).
-!- FUNCTION: Probably involved in cell adhesion. Receptor
alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poliovirus receptor related
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
                                                                                                                                                                                                                                    IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
                                                                                                                                                                                                        IsoId=Q15223-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF196769; AAG16648.1; OSINED. EMBL; AF196770; AAG16648.1; JOINED. EMBL; AF196771; AAG16648.1; JOINED. EMBL; AF196774; AAG16649.1; OSINED. EMBL; AF196769; AAG16649.1; OSINED. EMBL; AF196770; AAG16649.1; JOINED. EMBL; AF196771; AAG16649.1; JOINED. EMBL; AF196771; AAG16649.1; JOINED. EMBL; AF196771; AAG16649.1; JOINED. EMBL; AF196773; AAG16649.1; JOINED. EMBL; AF196773; AAG16649.1; JOINED. EMBL; AF196773; AAG16649.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF060231; AAC23798.1; --
EMBL; AY029539; AAK33124.1; --
EMBL; AF252867; AAG16648.1; --
EMBL; AF196768; AAG16648.1; JOINED.
EMBL; AF196770; AAG16648.1; JOINED.
EMBL; AF196771; AAG16648.1; JOINED.
EMBL; AF196771; AAG16648.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X76400; CAA53980.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 600644; -.
MIM; 225000; -.
MIM; 225060; -.
                                                                                                                                                                                         Name=Delta;
                                                                                                                                                                                                                      Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
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242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EKKAGPLGGS-----SYEE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| | | | : | | : | | : | | : | | EBEBEBGGGGGRRKVGGPHPKYDEDAKRPYFTVDBABARQDGYGDRTLGYQY---DPEQL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> KPRPORGIGSAARLLÄGTVAVFIJLVAVITVFFIYNRQ
QKSPPETDGAGTDQPLSQKPEPSPSRQSSLVPEDIQVVHLD
PGRQQQGEEDDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
ECP (in isoform Alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALRRRRHTFKGDYSTKKHVYGNGYSKAGI PQHHPPMAQNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPDDSDDEKKAGPLGGSSYEEEEEEEGGGGGERKVGGPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                           FPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 SLACIVNYHM--DRFKESLTLNVQYEPEVTIEGFDGNWYLQRMDVKLTCKADANPPATEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVALRRRRHTFKGDYSTKKHVYGNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QMCYQDRSPGKHHQNNDPKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK-----
                                                                                                                                                                                                                                                                                                                                      -> AFCQLIYPGKGRTRARMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                    (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                            (Potential)
                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                             (Potential) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.7%; Score 588; DB 1; Length 517; 30.1%; Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in isoform Alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform Gamma). /FTId=VSP 002625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DF34C8AEC893EE6D CRC64;
Ig-like v-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Poly-Glu.

Poly-Glu.

By similarity.

By similarity.

N-linked (GLONAC...) (()

N-linked (GLONAC...) (()

N-linked (GLONAC...) (()

N-linked (GLONAC...) (()

N-linked (GLONAC...) (()

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N-linked (GLONAC...) (()

N-linked (GLONAC...) (()
                                                                                                                                                                                                                                                                                                                                                          (in isoform Gamma).
/FTId=VSP_002624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 DLAENMVSQNDGSFISKKEWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 AA; 57158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similaily .....
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    517
  353
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530 AA;
                                                                                                                                                                                                                                                                                                                                                                                468
                                                                                                                                                                                Repeat; Signal
SIGNAL
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                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                               J. Virol. 73:4493-4497(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P22507-2; Sequence=VSP 002630, VSP 002631;
TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B (HveB)
                                                                  (Murine herpesvirus receptor homolog).
                                                                                                                                                             "Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene."; J. Virol. 66:2807-2813(1992).
                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G., "The murine homolog (Mph) of human herpesvirus entry protein B (H mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2.";
                                                                                                                                                                                                                        Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.; "Anhino acid residues on human poliovirus receptor involved in interaction with poliovirus."; J. Biol. Chem. 269:1431-6438 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        svent=Alternative splicing; Named isoforms=2;
                               P32507; Q62096;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 2 precursor
entry protein B) (mHveB) (Nectin 2) (Poliovirus
                         530 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P32507-1; Sequence=Displayed;
                                                                                   Name=Pvrl2; Synonyms=Mph, Pvr, Pvs;
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99214397; PubMed=10196354;
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM ALPHA)
                                                                                                                                                                                                  (ISOFORM BETA).
                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BETA)
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-94179228; PubMed-8132569;
                                                                                                                                              MEDLINE=92219365; PubMed=1560525;
                                                                                                                                                       Morrison M.E., Racaniello V.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS
                         STANDARD;
                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Beta;
                         PVR2 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVTWQRLDG---TVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGLR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 ILQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
ESPSTAGARGATGGILGGILAALIATAVAGTGILICROOKKE
ORLQAADEEEELEGPPSYKPPTPKAKLEEPEMPSQLFTLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRLQAADEEEELEGPPSYKPPTPKAKLEEPEMPSQLFTLGA
SEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGPLLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGLGP -> DTPQASRDVGPLVWGAVGGTLLVLLLAGGFL
ALILLRGRRRRKSPGGGGNDGDRGSYDPKTQVFGNGGPVFW
RSASPEPMRPDGREEDEEEEEEMKAEEGLMLPPHESPKDDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 VLPPSRLSPTLPLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
Potential.
Poliovirus receptor related protein 2.
Extracellular (Potential).
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                EMBL, BC05991; AAH99941.1; -.
PIR, A38211; HLMSP3.
PIR, A53427, A53427.
InterPro: IPR007110; Ig-like.
PROSTIR: PS0635; IG LIKE.
Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESHLDGSLISRRAVYV (in isoform Alpha)
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 19.9%; Score 540; DB 1; Length 530; Local Similarity 28.8%; Pred. No. 4.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (In isoform Alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0ED71BFA2B231BBE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57317 MW;
                                                                                                                                                                                                                                                                                                      EMBL; M80206; AAA39734.1; -. EMBL; D26107; BAA05103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 153; Conservative
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530
3351
3351
2247
2247
2250
3320
3128
3158
467
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

Alternol R.D., Colling F.S., Wagner L.H., Derge J.G.,

Alternol S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alternol S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alternol B.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

Villalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
295 PASAVAQGSQL-LVHSVDRMVHTFICTATNAVGTGRAEQVILVRESP--STAGAGATGG 351
                                                                                                         VIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL 423
                                                                                                                                            | : | | : | | | 412 PSQLFTLGASEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGPLLLGATGLGPSLLV 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                       POK--DLFOPEHLPLOTOF--------KEREVGNLQHSNGLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                        -----SRSFDYEDENPVGEDGIQQMYPLYNQMCYQDRSPGKHHQNND 497
                                                                                                                                                                                                                                                                                                                                                                                                                  | | : |: | : |: | : : | | : : | | 32 PPGPNVVEGVSLSLEDEEEDDEEDFLDKINPIYDALSYP--SPSDSYQSKD 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ODDKVLVATCTSANGKPPSVVSWETRLKGEAEYQEIRNPNGTVTVISRYRLVPSRFAHQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 588; DB 4; Length 514;
; Pred. No. 1.3e-46;
85; Mismatches 176; Indels
        US-08-659-984A-1

US-08-66-531-1

US-08-06-531-1

US-08-986-485-2

US-09-205-258-947

US-09-915-528-947

US-09-915-528-947

US-09-915-528-947

US-09-949-016-6213

US-09-949-016-7850

US-09-949-016-7850

US-09-949-016-7850

US-09-949-016-7850

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US-09-949-016-7850
                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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Best Local Similarity 30.1%;
Matches 151; Conservative
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APPLICANT: Universita degli Studi di Bologna
APPLICANT: Universita degli Studi di Bologna
APPLICANT: Institut National de la Sante et de la Recherche M
TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
TITLE OF INVENTION: BHV Infections
FILE REPERBUCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
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                                                                  461
                                                                                                                                                                                128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDY
                                                                                                           ----SYEE
                                                                                                                                                       EDENPVGEDGIQQM----YPLYN-----QMCYQDRSPGKHHQNNDPKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin
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General Functional Class of Gene:
Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding Macromolecules: HSV-gD
Subcellular localisation: Plasma
Other Information: Viral Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 21.6%; Score 584.5; DB 4; al Similarity 35.5%; Pred. No. 2.4e-46; 137; Conservative 67; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 SPPLPQKDLFQPEHL-PLQTQFKERE 444
                                                                                                           401 SKAGIPOHH--PPMAQNLQYPDDSDD
                                                                                                                                                                                                                                              -----YIDPREHYV 510
                                                                                                                                                                                                                                                                                         517
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09435956A Patent No. 6469155
                                                                                                                                                                                                                                                                                         496 DLAENMVSONDGSFISKKEWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: G;
OTHER INFORMATION: B:
OTHER INFORMATION: B:
OTHER INFORMATION: O:
US-09-435-956A-1
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Best Local Similarity
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LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTDVVLHCSFANPLPSVKITOVTWOKSTNGSKONVAIYNPSMGVSVLAPYRERVEFLRPS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
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  SPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVALRRRRHFKGDYSTKKHVYGNGY 397
                                                                  -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDY 461
                                                                                                                                                           -----QMCYQDRSPGKHHQNNDPKRV 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SPEAR, Patricia G.
APPLICANT: SPEAR, Patricia G.
APPLICANT: GERAGHIY, ROBERT G.
APPLICANT: GERAGHIY, ROBERT G.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: KRUMENACHER, Claude
APPLICANT: KRUMENACHER, Claude
APPLICANT: KRUMENACHER, Claude
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBERNER: Claude
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
TITLE OF INVENTION NUMBER: U.S. 60/087,862
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 26
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30.1%; Pred. No. 1.3e-46;
tive 85; Mismatches 176; Indels
                                                                                                                                                           EDENPVGEDGIQOM----YPLYN----
                                                                                                                                                                                                                                                ---YIDPREHYV 510
                                                                                                              SKAGI POHH - - PPMAQNLQYPDDSDD
                                                                                                                                                                                                                                                                                         493 DLAENMVSQNDGSFISKKEWYV 514
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09723368
Patent No. 6641818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NORTHWESTERN UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local S:
Matches 151
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Query Match
Best Local Similarity 29.6%
Matches 128; Conservative
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20.9%; Score 565.5; DB 4; Length 518;
Best Local Similarity 29.0%; Pred. No. 1.8e-44;
Matches 148; Conservative 85; Mismatches 171; Indels 107;
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US-09-919-172-20
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Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : | Y : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR SEQ ID NOS: 102
SOFTWARE: PERL Program
; Sequence 7563; Application US/09949016; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09919172
Patent No. 6673545
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ORGANISM: Homo sapiens
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APPLICANT: Faris, Mary
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LENGTH: 518
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RESULT 5

FEATURE:

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REPERBUCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-10-20
PRIOR PEPLICATION NUMBER: 60/21,755
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 7563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 IIVEPHVTAVWGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFSVQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 VTVLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHI------DWEGDL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GEMESTITISFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 VSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTF 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 LRVIAKPKNQAEAQKVTFSQDP-----TTVALCISKEGRPPARISWLSSLDWEAKE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 NYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA--VAGAVIGAVLALFIIA--IFV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 RPPQSGPRASGRAQSPPGPSMARAAALLPSRSPPTP----LLWPLLLLLLLLETGAQDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RIPGPSPLCPGGGKAQLSSASLLGAGLL--LQPPTPPPLLLLLFPLLLFSRL-CGALAGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.2%; Score 467.5; DB 4; Length 522; 29.6%; Pred. No. 3.2e-35; tive 69; Mismatches 180; Indels 55
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| Sequence 2. Application US/09723368 |
| Patent No. 6641818 |
| GENERAL INFORMATION: |
| APPLICANT: NORTHWESTERN UNIVERSITY |
| APPLICANT: SPEAR, Patricia G. |
| APPLICANT: GERAGHT, ROBERT G. |
| APPLICANT: GERAGHT, ROBERT G. |
| APPLICANT: MARNER, MONGOMERY, Rebecca I. |
| APPLICANT: COHEN, Gary H. |
| APPLICANT: EISENBERG, ROSELY J. |
| APPLICANT: HITBERCK, Charles J. |
| APPLICANT: KRUMMENACHER, Claude
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US-09-949-016-6278
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; Betent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VBTERE, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT PELLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR RELING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO S: 207012
; SEQ ID NO S: 207012
; SEQ ID NO S: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTVTSRFTLVPSGRADGV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIWORPDAPANHONVAAFHPKMGPSFPSPKPGSERLSFVSAKOSTGODTEAELQDATLAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PPTP----LLWPLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL 67
                                                                                                                                                                                                                                                                                                                                                                                                                        PPTPPPLLLLLFPLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290.0050/1050/723,368
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATCHLIN VET. 2.1
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t; Pred. No. 2e-34;
66; Mismatches 160;
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30.2%;
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Best Local Similarity 30.2°
Matches 121; Conservative
                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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ORGANISM: Human
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US-09-949-016-6278
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Sequence 7564, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-10-414
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2007012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                      128 HGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDP-----T 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 TVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDVRSNPEPTGY
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                                                                                                                    33 PPTPPPLLLLLPPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITQ
                                                                                                                                                                                                                                                                                                                                                             136 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBP-----TVSLIKGPDSLIDGGNET
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                                                        53;
Length 479;
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28.3%; Pred. No. 8.7e-30;
ive 70; Mismatches 184; Indels
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 ISSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
Query Match 16.9%; Score 458.5; DB 4;
Best Local Similarity 30.2%; Pred. No. 2e-34;
Matches 121; Conservative 66; Mismatches 160;
                                                                                                                                                                                                                                            89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF-
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Best Local Similarity
Matches 119; Conserv
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us-09-972-268-10.rai

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44 GSTTLHCSLTSNENVTITQITWMKKDSGGSHALVAVFHPKKGPNIKEPERVKFLAAQQDL 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 DAAGYNWSTUTGDFPUSVKRQGNMLLISTVEDGLNNTVIVCEVTNALGSGQGQVHIIVKE 335
                     129 NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLI--DG 184
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327 PLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGAVIGAVLALFIIAIFV 386
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                                                                                                                                                                                                                                                                           APPLICANT: Watson, James D
APPLICANT: Watson, James G
TITLE OF INVENTION: Polymuclectides, polypeptides expressed
TITLE OF INVENTION: By the polymuclectides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 400.5; DB 3; Length 30.8%; Pred. No. 4.6e-29; Live 64; Mismatches. 167; Indels
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TITLE OF INVENTION: Molecules Designated B7L1
PILE REFERENCE: 2844 US
CURRENT APPLICATION NUMBER: US/09/778,510
                                                                                                                                                                                                                    ; Sequence 62, Application US/09724864; Patent No. 6380362; GENERAL INFORMATION:
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US-09-778-510-20
'Sequence 20, Application US/09778510
'Patent No. 6512095
'GENERAL INFORMATION:
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Best Local Similarity 30.8*
Matches 123; Conservative
                                                                                387 TV 388
                                                                                                                    360 GI 361
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ORGANISM: Mouse
                                                                                                                                                                                                         US-09-724-864-62
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Sequence 6729, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER,

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14, 755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-00-03

SEQ ID NOS: 2070012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                 311 PPEVSISGYDNNWYLGQNEATLICDARSNPEPTGYNWSTTWGPLPPFAVAQGAQL-LIRP 369
                                                                                                                                                                                                                                                                                                                                  370 VDKPINTTLICNVTNALGARQAELTVQVKEGPPSEHSGMS-RNAIIFLVLGILVFLILLG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
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  TPPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGD 209
                                                                                                                                            LGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQY 267
                                                                                                                                                                                                                            268 APEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHP 327
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                                                                                       195 TFPQGSRSVDIWLRVLAKPQNTAEVQXVQLT----GEPVPMARCVSTGGRPPAQITWHSD
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Matches 106; Conservative
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US-09-949-016-6729
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CURRENT APPLICATION NUMBER: 2001-05-25
                             8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVT
                                                                                           3 SVVLPSGSOCAAAAAAPPGLRLR-----LLLLLFSA---AALIPTGDGQNLFTKDVT
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; Sequence 61, Application US/09866028
; Patent No. 6642360
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Grimaldi, Christopher
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Best Local Similarity 25.24
Matches 108; Conservative
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APPLICANT: Botstein, David
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Goddard, Audrey
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Tumas, Daniel
Wood, William
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Napier, Mary
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, ROGER
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2010-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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25.0%; Pred. No. 3.9e-20;
tive 78; Mismatches 173; Indels
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11.3%; Score 306.5; DB 4;
Best Local Similarity 25.0%; Pred. No. 3.9e-20;
Matches 106; Conservative 78; Mismatches 173;
Matches 106; Conservative 78; Mismatches 173;
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
SPRIOR FILING DATE: 22
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6596493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 106; Conservative
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                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                           SEQ ID NO 20
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Best Local 9
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FILE REFERENCE: P2548P1C1.

CURRENT APPLICATION NUMBER: US/09/944,457

CURRENT FILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-05-25

PRIOR FILING DATE: 00/06/9,334

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997
                                                                                                                                                     124 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLI 182
                                                                                                                                                                                   98 LNFSSSELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQXDTAV 155
                                                                                                                                                                                                                                           DGGNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPT 236
                                                                                                                                                                                                                                                                    295 ANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIY 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHVTAVWGRNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF 123
                                                                                                                                                                                                                                                                                                                             237 RFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNAD 294
| : | | : :: |: SVVLPSGSQCAAAAAA-----AAPPGLRLL---LLLES--AAALIPTGDGQNLFT 47
                                                                                          48 KDVIVIEGEVĀTISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQL 97
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APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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Patent No. 6734288
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Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Roy, Margaret
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; Pred. No. 6e-20;
76; Mismatches 167; Indels 77
               PRIOR APPLICATION NUMBER: 60/669, 470
PRIOR PLING DATE: December 17, 1997
PRIOR PILING DATE: December 18, 1997
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: FEBTUARY 9, 1998
PRIOR PILING DATE: FEBTUARY 9, 1998
PRIOR PILING DATE: FEBTUARY 9, 1998
PRIOR PILING DATE: FEBTUARY 9, 1998
PRIOR PILING DATE: PEDTUARY 25, 1998
PRIOR PILING DATE: PEDTUARY 25, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
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PRIOR PLING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PELICATION NUMBER: PCT/USOV/08439
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
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PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/USOS/0414
PRIOR APPLICATION PRIOR FEBRUARY 22, 2000
December 16
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ORGANISM: Homo Sapien
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155 LGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGNETVAAICIAATGKPVAHIDW-EGD--- 209
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                                                                                                                                                                                                                                                                                              269 GKPQPVMVTWVRVDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLY 327
                                                                                                                                                                                                  183 DGGNETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETATIISQYKLFPT 236
                                                                                                                                                                                                                                                                        237 RFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNAD 294
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                                                    64 PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF 123
                                                                                                                            124 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLI 182
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| : | | : ::|: SVVLPSGSQCAAAAA-----AAPPGLRLL---LLLFS--AAALIPTGDGQNLFT 47
                                                                           48 KDVIVIEGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQL
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TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
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BER: PCT/US99/17906
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CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR PILING DATE: 1990-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 423
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US-09-778-510-22
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Search completed: October 6, 2005, 09:44:22 Job time : 22.3581 secs

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Sequence 12, A
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Sequence 18, A
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
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Sequence 21, Appl
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Sequence 114, Appl
Sequence 114, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 219, Appl
Sequence 219, Appl
Sequence 27, Appl
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ALIGNMENTS

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Sequence 10, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Cofton, Timothy E.
APPLICANT: Cofton, Timothy E.
APPLICANT: Youakim, Adal
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE 1
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 510; Conservative
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Qy 181 LIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 Db 181 LIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 L1 LIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 Qy 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300 Db 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300 Qy 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGGNSDQKVIXISDVPF 360 Db 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGGNSDQKVIXISDVPF 360 QY 361 KGVSSIAVAGAVIGAVIALFITHIYHFVHPLTFNYSGVXICKVTNSLGGNSDQKVIXISDVPF 360 QY 361 KGVSSIAVAGAVIGAVIALFITHIYHFVHPLTFNYSGVXILDKVIDLPFTHKPPPLYYERS 420	Db 361	Application US/08972268 No. US20030044893A1 RMMATION: Baum, Peter R. Fanslow, William C. Lofton, Timothy E. Sorensen, Eric A. Youakim, Aeric A. Youakim, Aeric A. Youakim, Description of the Company of	Ouery Match Query Match Best Local Similarity 100.0%; Pred. No. 2.2e-195; Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 7 PSPLCPGGGKAQLSSASLLGAGLLLQPPTPPLLLLLFSRLCGALAGPIIVEPHV 66	Qy 67 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGEYDEKNY 126 bb 61 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRYLFKNY 120 Cy 127 SLNDATITLHNIGFSDSGKXICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGN 186 Db 121 SLNDATITLHNIGFSDSGKXICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGN 180 Qy 187 ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITC 246 Db 181 ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITC 240 Qy 247 VVKHPALEKDIRYSFILDIQYAPEVSYTGYDGNWFVGRKGVNLKCNADANPPFKSVWSR 306 Db 241 VVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSR 300
		QY 421 PPLPOKDLFOPEHLPLQTOFKEREVGHLOHSNGINSRSFDYEDENPVGEDGIOQMYPLYN 480 Db 421 PPLPQKDLFQPEHLPLQTQFKEREVGHLQHSNGINSRSFDYEDENPVGEDGIOQMYPLYN 480 QY 481 QMCYQDRSPCKHHQNNDPRRVYIDPREHYV 510 A81 QMCYQDRSPCKHHQNNDPRRVYIDPREHYV 510 Bb 481 QMCYQDRSPCKHHQNNDPRRVYIDPREHYV 510 CB 9972-268-12 Sequence 12, Application US/09972268 Publication No. US20030044893A1 GENERAL INFORMATION: APPLICANT: Farslow, William C. APPLICANT: APPLICANT: APPLICANT: Sorensen, Eric A. APPLICANT: AVOARIM, Adel TITLE OF INVENTION: NECTIN POLYNUCLEOTIDES, METHODS OF MAKING AND USE T FILE REFERENCE: 3101-A CURRENT APPLICATION NUMBER: US/09/972,268 CURRENT APPLICATION VUMBER: US/09/38,557 PRIOR FILING DATE: 2000-10-05	S	Query Match 99.3%; Score 2693; DB 10; Length 510; Best Local Similarity 99.6%; Pred. No. 1.9e-196; Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 1 MARTERPSPLCPGGGRAQLSSASLGAGLLLOPPTPPLLLLFPLLLFSRLCGALAGPI 60 Db 1 MARTERPSPLCPGGGRAQLSSASLGAGLLLOPPTPPPLLLLFFPLLLFSRLCGALAGPI 60 QY 61 IVEPHVTAVWGRAVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEVQGR 120 QY 61 IVEPHVTAVWGRAVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEVQGR 120 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 L

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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Sorensen, Exic A.
APPLICANT: Sorensen, Exic A.
APPLICANT: Sorensen, Exic A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TI
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TI
FILE REFERENCE: 3101-A
CURRENT FILING DATE: 2000-10-05
PRIOR RILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 510
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TQTSSIAVAGAVIGAVLALFIITVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYEERI
                              PPLPQKDLF-QPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLY
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llarity 89.2%; Pred. No. 1.4e-174;
Conservative 22; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: mus musculus
US-09-972-268-18
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Best Local Similarity
Matches 456; Conserv
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89.2%; Pred. No. 1.4e-174;
ive 22; Mismatches 31;
                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09959845
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GARERAL INPORMATION:
APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
TITLE OF INVENTION: Protein Nectin-3
TITLE OF INVENTION: Protein Nectin-3
; TITLE FERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2001-03-09
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                               RSPGKHHQNNDPKRVYIDPREHYV 510
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Best Local Similarity
Matches 456; Conserv
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US-09-959-845-4
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Sequence 19, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Fanslow, William C.

APPLICANT: Inctron, Timothy E.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: O'UURIN, Adel

ITILE REFERENCE: 310.4

CURRENT APPLICATION NUMBER: US/09/972,268

CURRENT FILING DATE: 2001-10-05

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Version 3.1

SEQ ID NO 189

SEQ ID NO 189

LENGTH: 438
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93.7%; Pred. No. 2.9e-153;
ive 12; Mismatches 15;
TITLE OF INVENTION: Protein Nectin-3
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/JP01/01871
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: 438
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Best Local Similarity 93.74
Matches 401; Conservative
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                                                                                             Sequence 31. Application US/0997268
| Sequence 31. Application US/0997268
| Publication No. US20030044893A1
| GENERAL INFORMATION:
| APPLICANT: Baum, Peter R. |
| APPLICANT: Cofton, Timothy E. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| APPLICANT: Soremen, Eric A. |
| FILE REFERENCE: 3101-A
| CURRENT FILING NUMBER: US/09/972, 268
| CURRENT FILING DATE: 2001-10-05 |
| PRIOR FILING DATE: 2000-10-05 |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 3.1 |
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        481 SQMCHQDRSPRQHHPRN-PERLYINPREHYV 510
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APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 428; Conservative
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ORGANISM: homo sapiens
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                                                                       RESULT 6
US-09-972-268-31
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US-09-972-268-16

US-09-972-268-16

Sequence 16, Application US/09972268

Publication No. US20030044893A1

SERVERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Daten, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TF FILE REPRENCE: 3101-4

CURRENT APPLICATION NUMBER: US/09/972,268

CURRENT APPLICATION NUMBER: 60/238,557

PRIOR APPLICATION NUMBER: 60/238,557

PRIOR SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

Language 1. 1. 2000-10-05

SEQ ID NO 16

Language 2. 2000-10-05

SEQ ID NO 16

Language 2. 2000-10-05

SEQ ID NO 16

Language 2. 2000-10-05

SEQ ID NO 16

Language 2. 2000-10-05
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    1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                               61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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APPLICANT: Baum, Peter R.
APPLICANT: Enablow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Soremen, Eric A.
APPLICANT: Soremen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE OF INVENTION: 101-0-05
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-10-05
PRIOR PRIOR PLING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Petentin version 3.1
SEQ ID NO 14
LENGTH: 595
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                                                                                       Length 438;
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86.8%; Pred. No. 2.2e-138;
tive 3; Mismatches 16; Indels 38
                                                                                     Query Match 78.4%; Score 2125; DB 10; Length Best Local Similarity 93.7%; Pred. No. 2.9e-153; Matches 401; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.8
Matches 375; Conservative
                        musculus
; TYPE: PRT
; ORGANISM: mus
US-09-972-268-19
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Db 361 TTTLQPTIQMHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALPIVLVS 420 Qy 384 IFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYBERSPPLP 424 :	RESULT 12 US-09-972-268-6 ; Sequence 6, Application US/09972268 ; Sequence 6, Application US/09972268 ; Publication No. US20030044893A1 ; GENERAL INFORMATION: ; APPLICANT: Baum, Peter R. ; APPLICANT: Fanslow, William C. ; APPLICANT: Forensen, Eric A. ; APPLICANT: Sorensen, Eric A. ; APPLICANT: Sorensen, Eric A. ; APPLICANT: OFTEN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND U. ; TILLE OF INVENTION: NAMER: US/09/972,268 ; CURRENT FILING DATE: 2001-10-05 ; PRIOR APPLICATION NUMBER: 60/238,557 ; PRIOR PELLING DATE: 2000-10-05 ; NUMBER OF SEQ ID NOS: 39 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 6 ; LENGTH: 549 ; TYPE: PRT ; ORGANISM: home sapiens US-09-972-268-6	Query Match 70.3%; Score 1906.5; DB 10; Length 549; Best Local Similarity 67.6%; Pred. No. 1.7e-136; Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;	Qy 1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLIFPLLLFSRLCGALAGPI 60	QY 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120	QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDS 180 	Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240	OY 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300 	Qy 301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGGRSDQKVIYISDVP- 359	QY 360	384
Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 Qy 241 GRRITCVYKHPALEKDIRYSFILDIQYAAFEVSYTGYDGNWFVGRKGVNLKCNADANPPFF 300 Db 241 GRRITCVYKHPALEKDIRYSFILDIQYAAFEVSYTGYDGNWFVGRKGVNLKCNADANPPFF 300 Qy 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360 Db 301 KGTSS 365 Db 361 KQTSS 365	RESULT 11 US-09-972-268-4 US-09-972-268-4 Sequence 4, Application US/09972268 Publication No. US20030044893A1 GENERAL INFORMATION: APPLICANT: Baum, Peter R. APPLICANT: Baum, Peter R. APPLICANT: Cofficen, Timothy E. APPLICANT: Corensen, Exic A. APPLICANT: Vouakim, Adel TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE OF ILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PRIOR APPLICATION NUMBER: 60/238,557 PROPER PROPE	; FEALURE: NOTHER INFORMATION: mucleotides 1-21 are from Mus musculus Nectin-3, the rest are fro; CTHER INFORMATION: m human Nectin-3 alpha US-09-972-268-4	Query Match 71.0%; Score 1924.5; DB 10; Length 549; Best Local Similarity 67.9%; Pred. No. 7.3e-138; Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;	QY 1 MARTPGPSPLCPGGGKAQLSSASILGAGILLQPPTPPPLLILLFPLLLFSRLCGALAGFI 60	Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120 	QY 121 VLFKOYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 L	QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240	QY 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300	Qy 301 KSVWSRLDGQWPDGLLASDWTLHFVHPLTFUYSGVYICKVTNSLGQRSDQKVIYISDVP- 359	360FKQTSSIAVAGAVIGAVLALFIIA

USE TH

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APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Foreign, Timothy E.
APPLICANT: Journal Eric A.
APPLICANT: Soronsen, Eric A.
APPLICANT: Soronsen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE OF INVENTION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 60/238,557
PRIOR PLILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
TENCIND: A14
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US-09-972-268-13
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70.2%; Score 1903.5; DB 1
Best Local Similarity 84.4%; Pred. No. 3.5e-136;
Matches 373; Conservative 7; Mismatches 43;
                                                                                                                                                                                                                              CYQDRSPGKHHQNNDPKRV----YIDPREHYV 510
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
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ITILE OF INVENTION: IG6 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2-097C-PC
CURRENT APPLICATION NUMBER: US/10/161,572
CURRENT FILING DATE: 2002-06-03
PRIOR PAPLICATION NUMBER: US 60/296,076
PRIOR PAPLICATION NUMBER: US 60/396,076
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-10
PRIOR APPLICATION NUMBER: US 60/318,733
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PELING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-21
PRIOR PILING DATE: 2001-10-21
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATCHIN VETSION 3.1
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                                                                                                                     64; Indels
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                                                                                                                                                                                                                            70.3%; Score 1906.5; DB:
67.6%; Pred. No. 1.7e-136,
iive 33; Mismatches 64,
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Publication No. US20030087266A1
GENERAL INFORMATION:
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Best Local Similarity 67.64
Matches 388; Conservative
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US-10-161-572-45
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Banslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 60/238,557
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 426
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70.0%; Score 1899; DB 10; Length 426;
Best Local Similarity 76.2%; Pred. No. 5.4e-136;
Matches 380; Conservative 10; Mismatches 33; Indels 76
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                             ; Sequence 15, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
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------DKGSSHHHHH 426
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ORGANISM: Artificial Sequence
RESULT 15
US-09-972-268-15
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Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
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The invention relates to a substantially purified nectinalpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding activity. The epithelial or migration activity, viral polypeptide binding activity. The epithelial or midration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, parcellular transport discorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenic condition of a tissue or a subject, such as condification or angiogenic condition of a tissue or a subject, such as schaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpeavirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3beta protein.
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                                                                                                                                                                                                                       Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                             Youakim A;
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100.0%; Pred. No. 7.8e-213;
ive 0; Mismatches 0;
                                                          Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 98-99; 141pp; English.
                                                             Lofton TE,
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nes 510; Conservative
                                                             Baum PR, Fanslow WC,
(IMMV ) IMMUNEX CORP
                                                                                                                       WPI; 2002-426103/45.
N-PSDB; AAD37445.
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QMCYQDRSPGKHHQNNDPKRVYIDPREHYV 510

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The invention relates to a substantially purified nectinalsha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as isolatemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                   Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothbelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein encoding amino acids from mouse nectin-3 protein and the rest form human nectin-3beta protein. Human nectin-3beta gene is located on chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human nectin-3beta protein"
                                                                                                                                                                                                                                                     Mouse nectin-3-human nectin-3beta fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Mouse nectin-3 pprotein"
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481 QMCYQDRSPGKHHQNNDPKRVYIDPREHYV
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27-AUG-2002
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                                                                                                                                                        AAE23285;
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1 PSPLCPGGGKAQLSSASILGAGLLQPPTPPPLLILLFPLLFFRLCGALAGPIIVEPHV
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larity 100.0%; Pred. No. 1.5e-210;
Conservative 0; Mismatches 0;
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les 504; Conserv
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                                                                                                                                                                                                                                                                                 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                                                    Length 510;
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                                                                                  Score 2693; DB 5;
Pred. No. 1.1e-211;
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on 29-AUG-2003 to standardise OS field)
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                                                                                    99.5%;
99.6%;
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                                                                         99.59
Best Local Similarity 99.67
Matches 508; Conservative
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                                          Sequence 510 AA;
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Indels

Length 504;

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486

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The invention relates to a substantially purified nectinialpha, beta, camma and nectin-4 polypeptides and their corresponding polynucleotides. CC gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial cor endothelial barrier function disorder which is treated by the above motorioned method is inflammation, sepsis, oceems, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, cathma, allergy, allograft rejection, metastasis of cancer cells, cathma, allergy, allograft rejection, metastasis of cancer cells, cathma, and angiogenesis in a mammal and treating endothelial migration, conjiferation or angiogenic condition of a tissue or a subject, such as includent and reating endothelial migration, conditions or a subject such as series, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell, (vascular semooth muscle cell). The present sequence is human nectin-3beta protein containing 6 amino acids deleted from the N-terminal end. Human nectin-3beta protein.
                                                                                                                                                                                                                                                   Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
Youakim
Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 89-91; 141pp; English
Lofton TE,
Fanslow WC,
                                                                                                   2002-426103/45
                                                                                                                                                                N-PSDB; AAD37443
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The invention relates to a substantially purified nectinialpha, beta,

gamma and nectin-4 polypeptides and their corresponding polymucleotides.

Nectin DNA and protein are useful for treating a disease associated with

cell adhesion activity, adherens junction formation activity, epithelial

cell adhesion activity, viral polypeptide binding activity. The epithelial

cell adhesion activity, viral polypeptide binding activity. The epithelial or

migration activity, viral polypeptide binding activity. The above

morthelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic relingathy,

paracellular transport disorders such as magnesium transport defects in

the kidney or inflammatory bowel disease. Nectin DNA is also useful for

the kidney or inflammatory bowel disease. Nectin DNA is also useful for

confiberation or angiogeneis in a mammal and treating endothelial migration,

proliferation or angiogenic condition of a tissue or a subject, such as

cischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

stroke, reserenceis, unmour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an

endothelial cell, an epithelial cell or a smooth muscle cell (vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                  480
                                                                                                   361 TÓTSSTAVAGAVIGAVLALFITTVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYEERI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; nectin-1beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                                                                                           361 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS
                                                                                                                                        421 PPLPQKDLF-QPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorensen EA,
                                                                                                                                                                                                                                  Disclosure; Page 109-110; 141pp; English.
                                                                                                                                                                                                               NOMCYODRSPGKHHONNDPKRVYIDPREHYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lofton TE,
                                                                                                                                                                                                                                                                                                                                           AAE23292 standard; protein; 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse nectin-3beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-426103/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
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                                                                                                                                                                                                                                    Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or diagnosing and treating tumor infiltration and the mouse nectin-3 protein families and
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Pred. No. 1.1e-186;
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                                                                                                                                                                                                  Amino acid sequence of murine nectin-3.
RSPGKHHQNNDPKRVYIDPREHYV 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 45-48; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISC-) JAPAN SCI & TECHNOLOGY CORP. (TAKA/) TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment and prevention of cancer
                                                                                        AAG63983 standard; protein; 510
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corresponding antibodies.
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                                                                                                                                                                                                                                                         GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                                                                                                                                                          TQTSSIAVAGAVIGAVLALFIITVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYEERI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, nectin-3gamma; therapy, cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease;
                                                                                                                                            61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
                                                                                                                                                                                                                                           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                           KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                                                                                                                                                                                                                                                                                                          KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYBERS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLPQKDLLGQTEHLPLQTQFKEKGAGGLQPSNGPISRRFDYEDESTMQEDGTQRMCPLY 480
                                                                                             9
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smooth muscle cell). The present sequence is mouse nectin-3beta protein
                                                                                                                                                          VLFKNYSLNDATITLHNIGPSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                             1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                    1 MARTPGPAPLCPGGGKAQLSSAFPPAAGLILPPPPPPPPLLLLLIPLLFSRLCGALAGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLPQKDLF-QPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLY
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oedema, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, tumour, cancer, herpesvirus infection, asthma, chromosome
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7
                                              510
                                                                     33; Indels
                                                Length
                                             Score 2388; DB 5;
Pred. No. 1.1e-186;
2; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOMCYODRSPGKHHONNDPKRVYIDPREHYV 510
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                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000; 2000US-0238557P.
                                              88.2%;
88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
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                                                                     454; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human nectin-3gamma
                                                          Similarity
                        Sequence 510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200228902-A2
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                                                Match
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                                                          Local
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                                                                    Matches
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gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, opithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedems, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting anglogenesis in a mammal and treating endothelial migration, well feration or and consideration or and consideration in the real paracellular properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                   purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, 1 for treating or preventing heart failure, malaria, rulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation or angiogenic condition of a tissue or a subject, such as ischemia, atherosclerosis, ischemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3gamma protein. Human nectin-3gamma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                                                           invention relates to a substantially purified nectin3alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 437;
Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.4%; Score 2257; DB 5; L 100.0%; Pred. No. 4.7e-176; Live 0; Mismatches 0;
Sorensen EA,
                                                                                                                                                                                   Claim 1; Page 125-126; 141pp; English.
Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.4
Best Local Similarity 100.
Matches 430; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430
                                                                                                           useful for treating or
glomerulonephritis, end
Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLPQKDLFQ
                                   WPI; 2002-426103/45.
N-PSDB; AAD37450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 437 AA;
                                                                                                                                                 sepsis, stroke
PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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RESULT 7

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The invention relates to a substantially purified nectinisalpha, beta,

C gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with

cell adhesion activity, adherens juuction formation activity, epithelial

cell adhesion activity, viral polypeptide bhinding activity. The epithelial

con endothelial barrier function activity, endothelial proliferation or

con endothelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

cendothelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

cendothelial paragraft rejection, metastassis of cancer cells,

centroling anglogents in a mammal and treating endothelial migration,

confinibiting anglogenesis in a mammal and treating endothelial migration,

confinibiting anglogenesis, ischaemia-reperfusion injury, thrombosis,

controling atherosclerosis, ischaemia-reperfusion injury, thrombosis,

stroke, restenosis, tumour growth and treating herpesvirus infection.

Nectin is also useful for modulating proliferation or migration of an

cendothelial cell, an epithelial cell or a smooth muscle cell (vascular

conducted in the present sequence is mouse nectin-3gamma protein
                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, nectin-3gamma, therapy, cell adhesion, cell proliferation, sepsis, paracellular transport disorder, kidney, diabetic retinopathy, allergy, allograft rejection, metastasis, restenosis, inflammatory bowel disease, oedema, atherosclerosis, ischemia reperfusion injury, thrombosis, stroke, tumour, cancer, herpesvirus infection, asthma.
361 IQTSSIAVAGAVIALFIITVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYEERI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGFI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 111-112; 141pp; English.
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                                                                                                                                                                                                                                AAE23293 standard; protein; 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000; 2000US-0238557P.
                                                                                                                                                                                                                                                                                                                                                                  Mouse nectin-3gamma protein.
                                                                                                               421 PSLPOKDL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV) IMMUNEX CORP.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200228902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                      27-AUG-2002
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                                                                       421
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                                                                                                                                                                                                                                                                          AAE23293
                                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR
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                                                                                                                                                                                    Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                          Amino acid sequence of murine nectin-3.
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    protein; 438
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TAKAHASHI K.
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Best Local Similarity 93.2
Matches 399; Conservative
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N-PSDB; AAH78181.
    AAG63984 standard;
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                                                                                                                                                                                              nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
                                                                                                                                                                                                                                                                                                                                                 paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                      GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                       IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

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Novel Durified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
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                                                                                                                     MARTLRESPLCPGGGKAQLSSASLLGAGLLLQPPTPLLLLLFPLLLFSRLCGALAGFI
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                                                89; Gaps
70.9%; Score 1920.5; DB 5; Length 549; 67.9%; Pred. No. 2.4e-148; ive 33; Mismatches 62; Indels 89;
                              Best Local Similarity 67.9
Matches 390; Conservative
                           Local Similarity
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                                                                                                                               ---FKQTSSIAVAGAVIGAVLALFIIA 383
                                              TTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
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kidney cancer;
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   Score 1920.5; DB 6
Pred. No. 2.4e-148;
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14-MAY-2003; 2003DE-01022134.
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Matches 390; Conservative
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(DAHL/) DAHL E.
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This invention describes novel cytostatic polymucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection with a prostatic tissue. Screening for inhibitors of the sequences or detection of substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligomucleotides, short-interferring RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide, in a petamer against the polypeptide, that binds to the polypeptide, so preferably humanised or human; an anti-idotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concernational with anti-human CD4 murine monoclonal antibodies; biocony strongly but non-malignant cells only waskly. In 15 of 63 samples were counterstained with hemalum (blue). Malignant cells stained second antibodiase accolur former (brown). The samples were counterstained with hemalum (blue) accolur former (brown), membrane and cytoplasmic staining was very strong, and encoarcinoma, membrane and cytoplasmic staining was very strong, invention
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3, Bruemmendorf T, Kinnemann H, Roepcke S;
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                                                                                                                                                                                                                New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
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Matches 390; Conservative
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Beckmann G,
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ROSENTHAL A.
HERMANN K.
PILARSKY C.
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Xinzhong L,
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(HERM/)
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KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359
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                                                                                                               --PPPLYEERSPPLP 424
                                                                                                                                                                        425 QKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQM 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel cytostatic polynucleotide and polypeptide
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                                                          ---FKQTSSIAVAGAVIGAVLALFIIA
                                                                                                                                            121 VLAGIFCYRRRRFFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPV-
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Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
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                                                                                                                                                                                                                                  483 CYQDRSPGKHHQNNDPKRV----YIDPREHYV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; cytostatic; diagnosis; prostatic cancer; differential expression analysis.
                                                                                                                 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHK----
                                                                                                                                                                                                                                                     Claim 2; Page 1205; 1607pp; German.
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                                                                                                                                                                                                                                                                                                                                     ADR66711 standard; protein; 549
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14-MAY-2003; 2003DE-01022134.
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                                                            DAHL E.
ROSENTHAL A.
HERMANN K.
PILARSKY C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004076614-A2.
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(HERM/)
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nectin-3beta-IgG1Fc region fusion protein.

(first entry)

27-AUG-2002

Нишап

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polypeptide, preferably humanised or human; an anti-idiody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that Drostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown) The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the
preferably 300, that binds
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Sequence 549 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                        384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHK---------PPPLYEERSPPLP 424
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                                                                                                   LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                                                    1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - NNLIRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYYEDLKMGMKFVSD--
                           89,
70.9%; Score 1920.5; DB 8; Length 549; 67.9%; Pred. No. 2.4e-148; ive 33; Mismatches 62; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYQDRSPGKHHQNNDPKRV-----YIDPREHYV 510
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               Local Simines 390;
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The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynuclectides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or endothelial barrier function activity, endothelial proliferation or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting anglogenesis in a mammal and treating endothelial migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemmia-reperfusion injury; thrombosis; gtroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy,
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Pred. No. 9.3e-148;
3; Mismatches 18;
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Best Local Similarity 86.3%;
Matches 373; Conservative 3
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                                                                                                KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                              KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                                                        KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420
VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                         GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                                                                                                                                                  Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
                                                                     GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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glomerulonephritis, endometriosis, leukemia, asthma, allergy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human nectin-3alpha protein"
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                                                                                                                                                                                                                                                                                                                Human nectin-3beta-FLAGpolyHis fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "FLAG peptide"
382. .387
/note= "PolyHis tag"
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Unidentified
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CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corremothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial correct function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, active kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, inhibiting angiogenesis in a mammal and treating endothelial migration, stochaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.

CR ischaemia, also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular prizer, reached). The present sequence is human nectin-3beta-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus inflection; asthma; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIXISDVPF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLLFPLLLFSRLCGALAGPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.6%; Score 1912; DB 5;
99.5%; Pred. No. 7.5e-148;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *LAGpolyHis fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.5
Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, astemnia, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular somoth muscle cell). The present sequence is a fusion protein containing mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3 alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARTPGPSPLCPGGGKAQLSSASLLGAGILLQPPTPPPLLLLLFPLLLFSRLCGALAGPI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a substantially purified nectin3alpha, beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 549;
                                                                                                                                                                                                                                                                                                                                            Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
                                                                                                                           /note= "Human nectin-3alpha protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.4%; Score 1906.5; DB 5 67.6%; Pred. No. 3.4e-147;
                                                                                                                                                                                                                                                                                                                                              Sorensen EA,

    . . 7
    /note= "Mouse nectin-3 protein"
    8. .549

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 80-82; 141pp; English.
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Lofton TE,
                                                                                                                                                                                                                                    05-OCT-2001; 2001WO-US031392
                                                                                                                                                                                                                                                                       05-OCT-2000; 2000US-0238557P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 67.6
Matches 388; Conservative
                                                                                                                                                                                                                                                                                                                                              Baum PR, Fanslow WC,
                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                2002-426103/45
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD37441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 549 AA;
                                                                                                                                                            WO200228902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sepsis, stroke
musculus
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 Mus muscu
Chimeric.
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Best Local S
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VLFKNYSLNDATITLANIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGFDS 180

121

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181

VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGFDS 180

 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240

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300
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181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                                    241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                                                                                                                                                                                                                                                             -----FKQTSSIAVAGAVIGAVLALFIIA 383
                                                                                                                                                                                                  301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIXISDPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 QKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQM
                                                                                            KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP-
                                                                                                                                                                                                                                                                                                                                 361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS
                                                                                                                                                                                                                                                                                                                                                                                           384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHK--------PPPLYEERSPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                421 VLAGIFCYRRRFFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483 CYODRSPGKHHONNDPKRV-----YIDPREHYV 510
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                                                                                                                                                                  301
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Search completed: October 6, 2005, 09:51:36 Job time : 86.2348 secs

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October 6, 2005, 09:42:42; Search time 16.7671 Seconds (without alignments) 2926.593 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                  Run on:
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US-09-972-268-12 2707 1 MARTLRPSFLCPGGGKAQLS......KHHQNNDPKRVYIDPREHYV 510 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	w	poliovirus recepto	PRR2 delta - human	virus re	PRR2 alpha - human	poliovirus recepto	poliovirus recepto			-H	irregular chiasm C	perlecan precursor	hypothetical prote	hemicentin precurs	OX-2 membrane glyc	Down syndrome cell	heparan sulfate pr	adhesion molecule	surface glycoprote	neural cell adhesi	myelin-associated	myelin-associated	elastic titin - hu	myelin-associated	myelin-associated	glial cell membran	coxsackie- and ade	B-cell adhesion pr
SUMMARIES	ID	0873	JC4024	A53437	I68093	HLMSP3	153960	B44194	A44194	RWHUPD	RWHUPA	A54017 .	A49448	A38096	T20992	T43290	A47639	T08851	S18252	JH0506	A45254	IJBONC	A61084	B33785	138346	BNRT3S	BNRT3	A58532	JC7780	JH0371
	g :	0	N	~	~	н	N	N	~	Н	Н	~	N	N	N	N	7	7	7	~	~	Н	-	N	~	Н	Н	7	~	0
•	Length	407	518	530	538	467	478	392	417	392	417	416	764	4391	5175	5198	274	1896	3707	588	588	853	626	637	7962	582	929	1001	365	847
\$ Query	Match	ന	20.9	19.9	19.5	17.3	16.8	15.4	15.4	14.9	14.9	12.1	8.5	7.6	•	7.3	6.9	6.7	9.9	•		•	•	6.5			6.5		6.3	
I	Score	1173.5	565.5	540	527	467	455	418	418	402	402	326.5	229.5	205.5	196.5	196.5	187.5	181.5	178.5	178	178	177.5	177	177	176	175	175	174	170.5	
Result	No.	1	6	m	4	ហ	9	7	œ	σ	10	11	12	13		15			18	19	20	21	22	23	24	25				29

RESULT 2 JC4024

OX-2 membrane glyc	neural cell adhesi	DM-GRASP precursor	neural cell adhesi	cell adhesion mole	cell adhesion mole	cell adhesion mole	vascular cell adhe	carcinoembryonic a	neural cell adhesi	SHP substrate-1 pr	neural cell adhesi	cell surface glyco	SHP substrate-1 pr	dutt1 protein - mo	kinase-like protei
TDRTOX	IJRTNC	JH0464	IJHUNG	C42632	B42632	A42632	JN0581	A36319	IJMSNG	JC5288	IJCHNL	I38049	JC5289	T30805	A39712
-1	, -1	~	-	~	~	~	~	~	-	N	-	0	N	~	N
278	828	587	761	765	812	932	739	702	725	509	1091	646	513	1612	1051
0.9	0.9	0.9	0.9	6.0	0.9	6.0	6.0	5.9	5.9	5.8	5.8	5.8	5.7	5.7	5.7
	5	162	162	162	162	162	161.5	160.5	160	157	157	156	155	154	153.5
162.5	162														

ALIGNMENTS

RESULT	1.1
T08732	
hypoth	hypothetical protein DKF2p566B0846.1 - human (fragment)
C; Date	C.bate: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 09-Jul-2004
C; Acce	
R;Otte	R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. gubmitted to the Drotein Semionse Database Mar. 1999
A;Refe	4
A; Acce	A;Accession: T08732
A; Mole	A; Molecule type: mRNA
A; Resident	A).Crossiques: 1-40/ (CLI). A.Crossiques-references: INVIDDOW-000412, BMDI.AI.OCO071
A, Expe	fetal kidney;
C;Gene A;Note	C,Genetics: A,Note: DKFZp566B0846.1
Quer	43.48;
Matc	similarity 0; Conservat
λõ	143 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAALCIAATGKPVA 202
QO	1 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAALCIAATGKPVA 60
ò	203 HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 262
qq	61 HIDWEGDLGEMESTTISPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 120
ò	263 LDIQYAPEVSVTGYDGNMFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL 322
qa	121 LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDWTL 180
δ	323 HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP359
ΟP	181 HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIXISDPPTTTTLQPTIQWHPSTADIEDLAT 240
δλ	360FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKV 403
QO	241 EPKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRFFRGDYFAKN 300
ζ	404 IDLPPTH
QQ	301 Y-IPPSDMQKESQIDVLQQDELDPYPDSVKKENKNPVNNLIRKDYLEEPEKTQWN 354
λŏ	447 NLOHSNGINSRSPDYEDENPVG 468
q	355 NVENLNRF-ERPMDYYEDLKMG 375

17,

65

251 234 311 294

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C;Accession: 168093
R;Eberle, F: Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
R;Eberle, F: Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
R;Eberle, T: 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Accession: 168093
A;Accession: 168093
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Accule type: mRNA
A;Residues: 1-538 <RES>
                                         A;Accession: A53437
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 cAGK>
A;Cross-references: UNIPROT: P32507; GB:D26107; NID: 9475017; PIDN: BAA05103.1; PID: 9825507
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN: 146664, NCBIP: 146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 FSDSGXYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 PSQLFTLGASEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGPLLLGATGLGPSLLV 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 SFEEPILLPVTLSVRYPPEVSISGYDDNWYLCRSEAILTCDVRSNPEPTDYDWSTTSGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LLQPPTPPPLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VLPPSRLSPTLPLLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 QVTWQRLDG---TVVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 VIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: Q92692; GB:S79172; NID:g1042204; PID:g1042205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SRSFDYEDENPVGEDGIQQMYPLYNQMCYQDRSPGKHHQNND 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 540; DB 2; Length 53 28.8%; Pred. No. 6.1e-32; ive 85; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 VEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPOSV-
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C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
A; Reference number: A53437; MUID:94179228; PMID:8132569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 28.8
Matches 153; Conservative
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poliovirus receptor mPVR - mouse
C;Species: Mus musculla (house mouse)
C;Species: Mus musculla (house mouse)
C;Accession: A53437
FAAAKi, 'O.; Kaike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with p
    poliovirus receptor-related protein precursor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: John-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999 C; Accession: John-1995 #sequence_revision 16-Jul-1995 #text_change 05-Nov-1999 R; Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Egen 155, 261-265; Jugs A; Title: Complementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle: Omplementary DNA characterization and chromosomal localization of a human shiftle of the chromosomal localization of a human shiftle of the chromosomal localization of a human shiftle of the chromosomal localization of the chromosomal shiftle of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the chromosomal localization of the ch
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
A;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Cross-references: GDB:583951
A;Cross-references: GDB:583951
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Reywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>F;1-30/Domain: signal sequence #status predicted companies: transmembrane #status predicted <MAT>F;356-379/Domain: transmembrane #status predicted <TMM>F;36-379/Domain: transmembrane #status predicted <TMM>F;36-379/S00main: #status predicted <MAT>F;36-379/S00main: #status predicted <TMM>F;36-379/S00main: #status predicted <TMM>F;36-379/S00main: #status predicted <TMM>F;36-379/S00main: #status predicted <TMM>F;36-379/S00main: #status predicted <MAT>F;36-379/S00main: #status predicted <MAT>F;36
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A; Molecule type: mRNA
A; Residues: 1-518 <LOP>
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Best Local Similarity 27.3%; Pred. No. 5.6e-31; Matches 151; Conservative 94; Mismatches 206; Indels 102; Gaps 21;	Matches 127; Conservative 57; Mismatches 171; Indels 36; Gaps
33 PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITO	Qy 30 LLQPPTPPPLLILEPPLILESRLCGALAGPITVEPHVTAVWGKNVSLKCLIEVNETIT 87
13 PPTPLIMPLLILILETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL 00 TGHDVTHAVGG OMNATHINAVGRANAGA NATE	QY 88 QISWEKIHGKSSQTVAVHPQYGFSVQGEYQRVLFKNYSLNDATITLHNIG 139
OF LEMBELLIANS OF LAWRENCE OF THE CONTROL OF THE CO	66 QVTWQRLDGTVVAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGLR
QY 136 HNIGFSDSGKXICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET 188	OY 140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDSLIDGGNETVAAICI 194
189 VAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLFPTRFARGR	QY 195 AATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHP 251 176 STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRXSLVPVGRADGVKVTCRVEHE 234
DD 179 TVALCISKEGRPPARISMLSSLDWEAKETQVSGTLAGTVTVTSRFTLVPSGRADGV 234 QY 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302 :	Qy 252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQW 311
Db 235 TVTCKVEHESFEEFALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDVRSNPEPTGY 294 Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVXICKVTNSLGQRSDQKVIXISDVPFKQ 362	Qy 312 PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIXISDVPFKQTSSIAV 368
295 DWSTTSGTFPTSAVAQGSQL-VIHAVDSLFNTTFVCTVINAVGMGRAEQVIFVRETPN 363 TSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPP-P	Qy 369 AGAVIGAVLALFIAIFVT-VLLTPRKKRPS 398
DD 352 TAGAGATGGIIGGIIAAIIATAVAATGILICRQQRKEQTLQGAEEDEDLEGPPSYKPPTF 411 OY 415 LYEERSPPLPOKDLFOPEHLPLQTOFKEREVGNLQHSNG 453	RESULT 6
412 KAKLBAQEMPSQLFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPLHPGA	IS3960 PRR2 alpha - human
OY 454LINSRSFDYED-ENPVGEDGIQQMYPLYNQMCYQDRSPGKHHQNND 497	C.Species: Homo sapiens (man) C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 C.Pecession: 153960
4/Z ISDGSFIEVERGFRAVEDVSDDLEDEGEEEEEKIDDRINFIIDADSISSFSDSIQG	Kibbelle, F.; Dubreull, F.; Mattel, M.G.; Devilara, B.; Lopez, M. 6. Meriels, 267-272, 1995 A.Title. The biman DRR2 gene, related to the biman noliovirus recentor gene (PVR), is th
528KGFVMSRAMYV	
RESULT 5 HLMSP3	AjStatus: preliminary; cranslated irom GB/EMBL/DDBJ AjMolecule type: mRNA AjResidues: 1-478 (RES> AjCross-references: UNIPROT:09UEI6; GB:S79171; NID:q1042202; PID:q1042203
or homolog pi sculus domest 93 #sequence 11	C;Genetics: A;Gene: PRK2alpha C;Superfamily: poliovirus receptor; immunoglobulin homology F;276-331/Domain: immunoglobulin homology <imm></imm>
R;Morrison, M.E.; Racaniello, V.R. J. Virol. 66, 2807-2813, 1992 A.Title: Molecular cloning and expression of a murine homolog of the human poliovirus re A;Reference number: A38211; MUID:92219365; PMID:1560525	Query Match Best Local Similarity 30.3%; Pred. No. 9.5e-26; Matches 121; Conservative 67; Mismatches 159; Indels 52; Gaps 13;
	33 PPTPPPLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITO
A;Cross-references: UNIPROT:P32507; GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786 C;Superfamily: politovirus receptor; immunoglobulin homology	13 PPTPLLMPLLLLLLETGAQDVRVQVLPEVRGQLGGTVELP
17. 26.	OY BY ISMEALHGASS-1019 HIGH SUCCESSION OF THE SU
F:46-354/Domain: extracellular #Status predicted <ext> F:47-133/Domain: immunoglobulin homology <imm1> F:47-231/Domain: immunoglobulin homology <imm2> F:27-232/Domain: immunoglobulin homology <imm3></imm3></imm2></imm1></ext>	QY 136 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVBPTVSLIKGPDSLIDGGNET 188 Db 128 HGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDPT 178
F:355-374/Domain: transmembrane #Status predicted <tmn> F;375-467/Domain: intracellular #Status predicted <tmt> F;375-467/Domain: intracellular #Status predicted F;54-131,174-229,274-320/Disulfide bonds: #Status predicted F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmt></tmn>	QY 189 VAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR 242
Query Match 17.3%; Score 467; DB 1; Length 467; Best Local Similarity 32.5%; Pred. No. 1.2e-26;	Qy 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302

12;

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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A43024; B31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Takeg
EMBO J. 9, 3217-3224, 1990
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A;Cross-references: GB:M24406
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble fc
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A;Map position: 19q13.2-19q13.2
A;Map position: 19q13.2-19q13.2
A;Map position: 27/1; 143/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell Sc, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A;Reference number: A90910; MUID:89168426; PMID:2538245
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                                                                                                                                                                                                                                                                                                                                                                                                 91 WEKIHGKSSOTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                             66 WSR-HGESGSMAVFHQTQGPNYSEPKRLEFVAARL--GTELRDASLRMFGLRVEDEGNYT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFKSVWSRLDGOWPDGLLASDNTLH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 FVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALF 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 PPLLLLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQIS
                                                                                                                                                                                                                                                                                                                                              10 PPLLITLLEL----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 WEGDLGEMESTITS--PPNETATIISQYKLPPTRPARGRRITCVVKHPALEKDIRYSFIL
                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                    Length 417;
                                                                                                                                                                                               Query Match 15.4%; Score 418; DB 2; Length 41 Best Local Similarity 30.6%; Pred. No. 4.2e-23; Matches 112; Conservative 64; Mismatches 162; Indels
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-417 <KOI>
A;Residues: 1-477 <KOI>
C;Superfamily: policvirus receptor; immunoglobulin homology
C;Reywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: The poliovirus receptor protein is produced both A,Reference number: $12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poliovirus receptor splice form delta precursor - human N;Alternate names: poliovirus receptor H20B C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P15151; BMBL:X64116
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Opoliovirus receptor (clone AGW-alpha-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A4194
B;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J;Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has AReference number: A4194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                            RESULT 7

944194

poliovirus receptor (clone AGM-delta-1) - green monkey
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey grivet)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
A;Title: A second gene for the African green monkey poliovirus receptor that has:
A;Reference number: A44194; MUID:93059651; PMID:1331508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDVRSNPEPTGY 294
                                                        VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF-K 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLLLTLLEL---SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID
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A,Residues: 1-392 <KOI>
A,Cross-references: UNIPROT:P32506; GB:S48817
C,Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                      362 QTSSIAVAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
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LLGIGV 363
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A; Status: preliminary
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F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-416 cCHA
A;Cross-references: UNIPROT:Q7M048; GB:L12025
B;Cross-references: UNIPROT:Q7M048; GB:L12025
A;Cross-reference number: A61206; MUD:91184910; PMID:2010233
A;Accession: A61206
                                                                                                                               transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - HGESGSMAVFHQTQGPSYSESKRLEFVAARL--GAELRNASLRWFGLRVEDBGNYTCLF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLGGMPNTSQVPGFLSGTVTVTSLMILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKFVAHIDWEG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGOWPDGLLASDNTLHFVH 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                 < PVRB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK
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                              A.Map position: 19413.2-19413.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; P;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F;21-343/Domain: extracellular #status predicted <BXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F;21-339,380-41/MINID homology <IMMI>
F;159-223/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.9%; Score 402; DB 1; Length 41'
29.3%; Pred. No. 6.3e-22;
ive 67; Mismatches 163; Indels
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                                                                                                                                                                                                                                                                                                                             :159-223/Domain: immunoglobulin homology <IMM2>;259-314/Domain: immunoglobulin homology <IMM3>
   A;Cross-references: GDB:120324; OMIM:173850
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A; Residues: 34-41, 'X', 43-53 < CH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.3%
Matches 106; Conservative
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RESULT 10

NAIdernate names: poliovirus receptor H20A

N/Alternate names: poliovirus receptor H20A

N/Alternate names: poliovirus receptor H20A

N/Alternate names: poliovirus receptor Deta

N/Alternate names: poliovirus receptor H20A

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

A.Accession: S12048; Al1990

A.Artile: The poliovirus receptor protein is produced both as membrane-bound and secreted A.References: UNIPROT:PISISI; UNIPROT:Q96BJI; EMBL:X64116; NID:g35809; PIDN:CAA454

A.Molecule type: DAA

A.Molecule type: DAA

A.Molecule type: DAA

A.Molecule type: Mumer, E.; Racaniello, V.R.

Cell 56, 855-865, 1999

A.Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expected number: A09010; MUID:89168426; PMID:2538245

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Molecule type: mRNA

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A.Molecule type: mRNA
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-392/Product: poliovirus receptor delta #status predicted <MAT>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-343/Domain: immunoglobulin homology <IMM1>
F;25-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;34-367/Domain: tammembrane #status predicted <TMN>
F;368-392/Domain: transmembrane #status predicted <ITMN>
F;368-392/Domain: intracellular #status predicted
F;368-392/Domain: sitracellular #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity 29.3'
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A;Gene: GDB:PVR; PVS
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A;Reference number: A33625; MUID:90078352; PMID:2687294
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: Il-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49448; S34129
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proje
A;Reference number: A49448
A;Accession: A49448
A;Accession: A49448
A;Ketlus: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-764 *RAMA
A;Residues: 1-764 *RAMA
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                                    cel
A,Note: the residue at position 9 is suggested to be glycosylated asparagine C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma C;Keywords: glycoprotein; membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPINYSWSTATGPLPNSTHPQENGSHLLISTVDDLNNTIFVCKAINALGSGQGQVTILV- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                          GFLGGSTVLHCSLASKDNVTÍTÓLTWMKRDPDGSPFRACLPPQEGPSISDPERVKFLVAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYEDLRNASLAISNLRVEDEGIYECQIATPPTGSKSANVWLKVFARPKNTAEALEPSPTL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 IDGGNETVAAICIAATGKPVAHIDW----EGDLGEMESTTTSFPNETATIISQYKLFPTR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
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                                                                                                                                                                                                                                                                                             AVWGKNVSLKCLI--EVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 LLLLFPLLLFSRLCGAL-AGP-----IIVEPH-VTAVWGKNVSLKCLIEVNETITQI
                                                                                                                                                                                                                                                         SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLPPLLLFSRLCGALAGPIIVEPHVT
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                                                                                                                               Length 416;
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                                                                                                                                                                                           Indels
                                                                                                                               5;
                                                                                                                                                                                           56; Mismatches 171;
                                                                                                                         12.1%; Score 326.5; DB 2 28.1%; Pred. No. 2.3e-16;
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A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                           Matches 104;
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Best Local
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NyAlternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate protec Cippecies: Homo sapiens (man)
Cippecies: Homo sapiens (man)
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Cipate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004
Airtle: Primary structure of the human heparan sulfate proteoglycan from basement membra Airtle: Primary structure of the human heparan sulfate proteoglycan from basement membra Airtle: Authorize 138096; MuID:92235084; PMID:1569102
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A; Residues: 1.57, 'D', 59-434,'A', 436,'FL', 438-449,'Q', 451-502,'A', 503-792,'K', 794-908,'R',
A; Residues: 1.57,'D', 59-434,'A', 13169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-46]
A; Cross-references: EMBL, X62515; NID: 929469; PIDN: CAA44373.1; PID: 929470
B; Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.
Genomics 11, 389-396, 1991
A; Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the gent A; Reference number: A41059; MUID: 92120660; PMID: 1685141
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A; Molecule type: mRNA

A; Residues: RT', 1892-908, RK, 910-1101, LL', 1103-1132, 'L', 1134-1221,'L', 1223-1397 < RA2>

A; Residues: RE', 1892-908, RK, 910-1101, 'L', 1103-1121, 11, PID: 124371

R; Dodge, G.R.; Rovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F

B; Dodge, G.R.; Rovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F

B; Dodge, G.R.; Rovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F

A; Title: Heparan sulfate proceedylycan of human colon: partial molecular cloning, cellulan

A; Reference number: A40306; MUID: 91365376; PMID: 1679749
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*Residues 1.57, 'D',59-434,'A',436,'FL',438-449,'Q',451-502,'A',503-792,'K',794-908,'R',
71-2979,'H',2881-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-35
A;Cross-references: EMBL:X62515
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A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425
R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 109, 3199-3211, 1989
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A;Residues: 1-4391 <MUR>
A;Cross-references: UNIPROT:P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
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A;Reference number: A41736; MUID:92112994; PMID:1730768
                                                                                                                                                                                              289
                                                                                                                                                                                                                                                                                                                                                                                                       290 KCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYI-CKVTNSLGQRS 348
254
VAHIDWEGDLG----EMESTITSFPNETA-TIISQYKLFPTRFARGRRITCVVKHPALE
                                                                                               163 AÁEITWIDGLGNVLTDNIEYTVIPLÞDQRRFTAKSVLRLTPKKEHHNTNFSCQAQNTA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 ECRADANPSDVRYRWFIND----EPIIGGQKTEMVIRNVTRKFHDAIVKCEVQNSVGKSE
                                                                                                                                                                                                                                                             349 DQKVIYISDVP-FKQTSSIAVAGAVIGAVLAL 379
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submitted to the EMBL Data Library, October 1991
A;Reference number: S77946
A;Acferesion: S77946
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J. Cell Biol. 116, 559-571, 1992
A,Title: Human basement membrane
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 Hsequence revision 11-Jan-2000 Htext_change 09-Jul-2004
C;Accession: T43290; T20993; T24734
R;Vogel, B.B.; Hedgecock, B.M.
submitted to the EMBL Data Library, June 1998
A;Pescription: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-A;Reference number: Z22396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PVGRKGVNLKCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892 VPPEEQLIEGODLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLL 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEFTVSL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NLLITDAQI-----EDQGQFTCIARN-TYGQQSQSTTLMVTGLVSPVLGH 891
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGE
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A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: UNIPROT:076518; EMBL:AF074901; PIDN:AAC26792.1
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                                                                                                R;Sulston, J. Submitted to the EMBL Data Library, December 1994 submitted to the EMBL Data Library, December 1994 A;Reference number: 219355 A;Accession: T20992 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1994
A;Reference number: 219929
A;Accession: T24733
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                                                                      C; Accession: T20992; T24733
                                                                                                                                                                                                                                                                                   A; Residues: 1-5175 <WIL>
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Best Local Similarity
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                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                R; Kershaw, J.
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F)3886-3921/Domain: EGF homology <EGF>
F)3886-3921/Domain: EGF homology <EGF>
F)3886-3921/Domain: EGF homology <EGF>
F)3497-4175/Domain: EGF homology <EGF2>
F)4149-4151/Region: motor neuron attachment (L-R-E) motif
F)4299-4301/Region: motor neuron attachment (L-R-E) motif
F)57.1.77(Binding site: heparan sulfate (Ser) (covalent) #status predicted
F)895,534.1755,2121,3072,3105,3279,3780,3886,4068/Binding site: carbohydrate (Asn) (coval F)295,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                          A;Map position: 1p36.1-1p36.1
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembra
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-4391/Product: perlecan #status predicted <MAT>
F;22-193/Domain: I <DOM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3128 KAVTLEC-VSAGEPRSSARWTRISSTPAKLEORTYGLMDSHAVLO-ISSAKPSDAGTYVC 3185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPIIVE---PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQ 114
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                                                                                                                                                                                          of sequence shown
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F:199-234/Domain: LDL receptor ligand-binding repeat homology < LDL1>
F:285-319/Domain: LDL receptor ligand-binding repeat homology < LDL2>
F:325-359/Domain: LDL receptor ligand-binding repeat homology < LDL2>
F:326-359/Domain: LDL receptor ligand-binding repeat homology < LDL3>
F:368-403/Domain: LDL receptor ligand-binding repeat homology < LDL4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
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      A;Accession: B33625
A;Aolecule type: protein
A;Aocession: A33625
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A;Residues: 2166-2171, X', 2173-2175, X', 2177-2185 (HE3>A;Note: peptide potentially matches four different regions A;Genetics:
A;Genetics:
A;Genetics:
A;Cross-references: GDB:126372; OMIM:142461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1159-1206/Domain: laminin-type EGP-like homology <LEG>F;1563-1610/Domain: laminin-type EGF-like homology <EG7>F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
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F;2007-2034/Domain: transmembrane #status predicted <TRM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;531-1676/Domain: III <DOM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;3687-4391/Domain: V < DOM5>
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submitted to the EMBL Data Library, December 1994

A;Reference number: 219355

A;Accession: T20993

A;Accession: Preliminary; translated from GB/EMBL/DDBJ

A;Croser-ferences: EMBL:247068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A;Residues: 1-5198 «WIL»

A;Residues: 1-5198 «WIL»

A;Rershaw, J.

S;Rershaw, J.

S;Re
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121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 67.9%; Pred. No. 3.4e-136;
Matches 390; Conservative 33; Mismatches 62; Indels 89;
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Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;
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01-077-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                           GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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J. Biol. Chem. 275:10291-10299 (2000).
MBL; AR195833. AAF63687.1;
GO; 0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:integral to membrane; TAS.
GO; GO:0005515; F:proteain binding; IPI.
GO; GO:0005515; P:proteain binding; IPI.
GO; GO:0016317; P:cell-cell adhesion; IDA.
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361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
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                                                                                                                                 -----FKQTSSIAVAGAVIGAVLALFIIA 383
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                                                                                                                                                                                                                                                                                   VLAGIFCYRRRRFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKNPV- 478
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPRU0, 19; 1.
SMART; SM00409; IG; 1.
SMART; PSS0835; IG LIKE; 3.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Cell adhesion molecule nectin-3 alpha.
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Pred. No. 8.9e-133;
0; Mismatches 1;
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68.2%; Pred. No. 1.4e-128;
iive 35; Mismatches 60;
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EMBL: AF195833; AAF63685.1; --
MGD; MGI:1930171; Pyrl3.
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SEQUENCE 549 AA; 60582 MW;
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InterPro; IPR007110; Ig-like.
ilarity 99.7%;
Conservative
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SMART; SM00409; IG; 1
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610301B19 product:poliovirus receptor-related
3, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                  STRAIN=CS7BL/67; TISSUE=Whole body; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; Hiqshicaki Y.; Melth-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                             GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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                                                                       LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                           549 AA.
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Phudab S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
M. Marayama T., Miyazaki M., Nighi K., Nomura K., Numzaki R., Ohno M.,
Angayama T., Miyazaki A., Nighi K., Nomura K., Numzaki R., Ohno M.,
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Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AKO11949; BAB27933.1; -.
BMBL, AKO11949; BAB27933.1; -.
BMBL, AKO11949; BAB27933.1; -.
BMBC GO: GO:0005615; C:extracellular space; TAS.
GO: GO:001621; C:integral to membrane; TAS.
GO: GO:0016317; Procell adhesion; IDA.
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SEQUENCE FROM N.A.
SPRAINTE-20499374; PubMed=11012159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11012159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=1072159; DOI=10.1101/gr.145100;
Carninoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
Prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

C STRAIN=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
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InterPro; IPR007110; Ig-like.
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Best Local Simil
Matches 361; C
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241 EPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRFFRGDYFAKN 300
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SEQUENCE FROM N.A.
TISSUE-Kidney,
Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALGS 50071; CAB43256.1; -.
EMBL, T08732, T08732.
InterPro: IPR007110; Ig-like.
PROSITE; PSS0835; IG-LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.4%; Score 1173.5; DB 2; Length 407; 62.8%; Pred. No. 5e-80; ive 28; Mismatches 51; Indels 63;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation u
Hypothetical protein DKFZp566B0846 (Fragment)
Name=DKFZp566B0846,
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(TrEMBLrel. 17, I
(TrEMBLrel. 25, I
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Matches 240; Conservative 2
                                                                                                                            267
                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q9BVA9;
01-JUN-2001 (9
01-JUN-2001 (7
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301 KSVWRRLDGOWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGORSDOKVIYISDVPP 360
301 KSVWSRLDGOWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGORSDOKVIYISDPPP 360
GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300
                                                                                                                                                                                                                                            361 KQT-----VAGAVIGAVLALFIIA 383
                                                                                                                                                                                                                                                                                  384 IFVTVLLTPRKKR------PSYLDKVIDLPPTHK-----PPPLYEERSPPLPQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                               421 ILAGVFCYRRRRFRGDYFAKNYIPPSDMQKESQIDVLHQDBLDSYPDSVKKENKNPV-- 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LLRGPLLPRSFSGNPRALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS 75
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Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suziki Y., Nagai K., Sugano S., Ishila S., Kawai-Hio Y., Salto K., Yamanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX075105; BAC11404.1; -. GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR003599; Ig.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ90624.
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Best Local Similarity 96.09
Matches 242; Conservative
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Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867; Menotti L., Loppez M., Avitabile E., Seefan A., Cocchi F., Adelaide J., Leccoq E., Dubreuil P., Campadelli-Fiume G.; "The murine homolog of human nectini delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD."; proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                      CVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWS
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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QUAKF6; QUELLS; QUII7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
Name=Pvrl1; Synonyms=HveC, Prrl;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                        89;
                                                                                                                                                                                                                                                                                                                           24.0%; Score 648.5; DB 2; Length 304; 44.1%; Pred. No. 1.3e-40; ive 33; Mismatches 62; Indels 89.
                                                                                                                                                                Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       NON TER 1 1
SEQUENCE 304 AA; 34826 MW; BBEAACF94A6BA745 CRC64;
  to nectin 3; DKFZP566B0846 protein (Fragment).
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MEDLINE=20541977; bubmed=11090177;

DOI=10741274.24.11773-11781.2000;
Shukla D.; Dal Canto M.C.; Rowe C.L., Spear P.G.;
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                                                                                                                                                                                                   EMBL, BC001336, AAH01336.1; -.
InterPro; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.1%;
Matches 145; Conservative 3
                         Homo sapiens (Human)
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                                                                             NCBI_TaxID=9606;
                                                                                                                                             TISSUE=Cervix;
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Poly-Glu.

Poly-Glu.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

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N-linked (GlcNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.
SIGNAL, 1 30
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ilarity 30.4%; Pred. No. 8.8e-37;
Conservative 90; Mismatches 162; Indels 100; Gaps
"Striking similarity of murine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
                                                                                                                                                                                                                         Zhan J., Wimmer E.;
"Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in
floor plate during embryogenesis, suggesting a role in neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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N -> D (in Ref. 1).
P -> PP (in Ref. 2).
S -> G (in Ref. 3).
%; FFFG08EBSFFB7A0F CRC64;
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GO; GO:0005913; C:cell-cell adherens junction; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; IDA.
InterPro; IPR007110; IG-like.
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EMBL, AF270977; AAF76195.1; -.
EMBL, AF297665; AAG22808.1; -.
                                                                                               Virol. 74:11773-11781(2000).
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SEQUENCE TISSUB=Brain;

STRAIN=C57BL/6; TISSUB=Brain;

MEDLINE=2238625; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Itschul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A Itschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soares M.B., Bonaldow M.F., Carannor P.L., Scheetz T.E.,

B Brownstein M.J., Usdin T.B., Tocahlyuki S., Carannor P.L., Frange C.,

R Brownstein M.J., Usdin T.B., Tocahlyuki S., Carannor P., Prange C.,

B Robar S., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

Mitting M., Marra M.A., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Dones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                            FIDGTIRLSGLELEDEGMYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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DENPVGEDGIQQM---YPLYN-------50MCYQDRSPGKHHQNNDPKRV-- 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 GKNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 KAGIPQHH--PPMAQNLQYPDDSDD-----SYKRAGPLGGS-----SYEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GTDVVLHCSFANPLPSVKITQVTWQKASNGSKQNMAIYNPTMGVSVLPPYEKRVEFLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 TSS-----IAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
R Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

R Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005913; C:cell-cell adherens junction; IDA.

GO; GO:0005513; C:extracellular space; TAS.

R GO; GO:0005515; C:extracellular space; TAS.

R GO; GO:0004872; F:procein binding; IPI.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R SMART; SM00409; IG.2.

R SMART; SM00409; IG.2.

R SMART; SM00409; IG.2.

R SMART; SM00409; IG.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%; Score 598; DB 2; Length 51
31.0%; Pred. No. 1.8e-36;
ive 86; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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302

362

442 425 486

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262 RMDVKLTCKADANPPATEYHWTTLNGSLPKGVEAONRTLFFRGPINYSMAGTYICEATNP 321
                                                                                                                                                                                                              344 LGQRSDQKVIYISDVPFKQTS-----SIAVAGAVIGAV-LALFIIAIFVTVLLTP 392
                                                                                                                                                                                                                                                                                                                                                                                                          426 KKAGPL----GGSSYEEEEEEEGGGGERKVGGPHPKYDEDAKRPYFTVDEAEARQDGYGD 481
                                                          TATIISQYKLFFTRFARGRRITCVVKHPALEKDIRYSF1LD1QYAPEVSVTGYDGNWFVG
                                                                                                                                    RKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS
                                                                                                                                                                                                                                                                                          393 RKK-RPSYLDK------VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKE
                                                                                                                                                                                                                                                                                                                                                                    443 REVGNIQHSNGINSRSFDYEDENPVGEDGIQQMYPLYN--------OMCYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "cDNA characterization and chromosomal localization of a gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE-20392396; PubMed=10932188; DOI=10.1038/78119; Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by poliovirus receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-98279152; PubMed-9616127; DOI=10.1126/science.280.5369.1618;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015223; 075465; Q9HBE6; Q9HBW2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G; Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C., Dubreuil P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM GAMMA).

MEDLINE=21256041; PubMed=11356977;

DOI=10.1128/JVI.75.12.5684-5691.2001;

Lopez M., Cocchi F., Avitabile B., Leclerc A., Adelaide J.,

Campadelli-Fjume G., Dubreuil P.;

"Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectinl (or pri-HIGR-Hvec) modulates positively and negatively gusceptibility to hav infection.";

J. Virol. 75:5684-5691(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                382 RHTFKGDYSTKKHVYGNGYSKAGIPQHH--PPMAQNLQYPEDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 RSPGKHHQNNDPKRV------YIDPREHYV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Entry of alphaherpesviruses mediated protein 1 and poliovirus receptor."; Science 280:1618-1620(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the poliovirus receptor gene.";
Gene 155:261-265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PVRL1; Synonyms=HVEC, PRR1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CD111 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spear P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVR1 HUMAN
                                                            224
                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
PVR1 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCGALAGPIIVEPHVTAVWGKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 EPTVSLIKGPDSLIDG----GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig, 2.
SMART; SM00406; IGv.
PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                            is a functional alphaherpesvirus receptor.";
Virology 281:315-328(2001).
-!- FUNCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                        "Porcine HveC, a member of the highly conserved HveC/nectin 1 family
                                                                                                                                                                                                                                                                                          SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity) SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poliovirus receptor related protein 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential).
(Potential).
(Potential).
(Potential).
                    Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                    MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
                                                                                                                            Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linked (GlcNAc. . .) (P
BFAB00320DDE3785 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GlcNAc. . .)
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8.4e-36;
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C2-type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GlcNAc.
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Ig-like C2-type
Ig-like C2-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
N-linked (GlCN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; Score 589; 30.2%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
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N-linked
N-linked
N-linked
N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poly-Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.2%; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF308632; AAG30281.1; -. HSSP; Q05793; 1GL4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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202
202
286
286
3307
332
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SIGNAL 1
                                        Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307
332
515 AA;
                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                              SEQUENCE FROM N.A.
                                                            NCBI_TaxID=9823;
      scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                           Isold-015223-3; Sequence=VSP 002624, VSP 002625;
Isold-015223-3; Sequence=VSP 002624, VSP 002625;
DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
ectodermal dysplasia syndrome (CLPED1) [MIN:22500]. CLPED1 is
dysplasia [MIN:225060] and Zlotogora-Ogur syndrome.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
                                                        Dener. 20144/-1301/2000).
- UNDCTION: Probably involved in cell adhesion. Receptor for alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                  SUBUNIT: Interacts with HSV glycoprotein D (gD).
SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and

    Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.

    1
    30

    Potential.
    31

    STATOAL
    31

    STATOAL
    517

    Pollovirus receptor related protein 1.

    SOMAIN
    31

    355
    Extracellular (Potential).

             cell-cell adhesion
in cleft lip/palate-ectodermal
                                                                                                                                                                                                      IsoId=015223-2; Sequence=VSP_002626, VSP_002627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0005912; C:adherens junction; NAS.
GO; GO: 0015021; C:integral to membrane; NAS.
GO; GO: 0015026; P: coreceptor activity; TAS.
GO; GO: 0016337; P: cell-cell adhesion; NAS.
GO; GO: 0006955; P:immune response; NAS.
GO; GO: 0046718; P:viral entry; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
PRAMT; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Alternative splicing; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential)
                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                              IsoId=Q15223-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
                                                                                                                           delta). Secreted (isoform gamma). ALTERNATIVE PRODUCTS:
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JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X76400; CAA53980.2; ALT_INIT.
EMBL; AF060231; AAC23798.1; -.
EMBL; AX029539; AAK33124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED
Helms J.A., Spritz R.A.;
"Mutations of PVRL1, encoding a ce
molecule/herpesvirus receptor, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF196771; AGG6648.1; JO
EMBL, AF196774; AGG16649.1; --
EMBL, AF196769; AAG16649.1; JO
EMBL, AF196769; AAG16649.1; JO
EMBL, AF196770; AAG16649.1; JO
EMBL, AF196771; AAG16649.1; JO
EMBL, AF196772; AAG16649.1; JO
EMBL, AF196773; AAG16649.1; JO
                                                   25:427-430(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:9706; PVRL1.
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31
356
377
                                                                                                                                                                  Name=Delta;
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                                       dysplasia.";
Nat. Genet.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |:| | |: |: |: || |: |: 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402
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QKSPPETDGAGTDQPLSQKPEPSPSRQSSLVPEDIQVVHLD
PGRQQQGEEEDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
FCP (in isoform Alpha).
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YPDDSDDEKKAGPLGGSSYEBEBEBEBGGGGGBRKVGGPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 SLACIVNYHM--DRFKESLTLNVQYEPEVTIEGFDGNWYLQRMDVKLTCKADANPPATEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | : | | | 341 SPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVALRRRRHTFKGDYSTKKHVYGNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QMCYQDRSPGKHHQNNDPKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK-----
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                                                                                                                                                                                                                                                                                                                                                                  -> AFCQLIYPGKGRTRARMF
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                                                                                                                                                                                                                          (Potential). (Potential). (Potential).
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(Potential).
(Potential).
                                                                                                                                                                                                       (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FIId=VSP 002626.
Missing (In isoform Alpha).
/FIId=VSP 002627.
                                                                                                                                                                                                                                                                                                                                                                                     (in isoform Gamma).
/FTId=VSP 002624.
Missing (In isoform Gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DF34C8AEC893EE6D CRC64;
Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 1.

Ig-like C2-type 2.

Poly-Glu.

Poly-Glu.

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By similarity.

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Transmembrane.
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Matches 153; Conservative
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SIGNAL
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274
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CARBOHYD
VARSPLIC
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Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Carannor P.E., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toonhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Virol. 73:4493-4497(1999).
-!- FUNCTION: Receptor for alphaherpesvirus (such as murine HSV) entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold-P33507-2; Sequence-VSP 002630, VSP 002631;
TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
"The murine homolog (Mph) of human herpesvirus entry protein B (HveB)
mediates entry of pseudorabies virus but not herpes simplex virus
types 1 and 2.;
                                   PVR2_MOUSE STANDARD; PRI; 530 AA.
P32507; 062096;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (MHVeB) (Nectin 2) (Poliovirus receptor homolog).
                                                                                                                                                                                                                        MEDLINE=92219365; PubMed=1560525;
Morrison M.E., Racaniello V.R.;
Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene.";
Journal, 66:2807-2813(1992).
                                                                                                                              Name=Pvrl2; Synonyms=Mph, Pvr, Pvs;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM BETA).
STRAIN=FVB/N; TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                         Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A., "Amino acid residues on human poliovirus receptor involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P32507-1; Sequence=Displayed;
                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM BETA).
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=94179228; PubMed=8132569;
                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 269:8431-8438(1994)
                                                                                                                                                                                                                                                                                                                                                                         interaction with poliovirus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                               Aoki J., Koike S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            into cells.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).

1g-like V-type.
1g-like C2-type 1.
1g-like C2-type 2.
By similarity.
By similarity.
N-linked (GlCNAc. . ) (Potential).
N-linked (GlCNAc. . ) (Potential).
ESPSTAGAGATGGIIGGIIAAIIATAVAGTGIILCRQORKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPQSV------AVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRLQAADEBEBLEGPPSYKPPTPKAKLEBPBMPSQLFTLGA
SEHSPVKTPYFDAGVSCADQEMPRYHELPTLEBRSGPLLLG
ATGLGP -> DTPQASRDVGPLVWGAVGGTLLVILLLAGGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALILLRGRRRRKS PGGGGNDGDRGSYDPKTQVFGNGGPVFW
RSASPEPMRPDGREEDEEEEEMKAEEGLMLPPHESPKDDM
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC05991; AAH59941.1; -.
PIR; A3821; HLMSP3.
PIR; A53437.
A51437.
InterPro; IPR007110; Ig-like.
PROSTIE: PS50835; IG LIKE; 3.
Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poliovirus receptor related protein 2. Extracellular (Potential).
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-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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28.8%; Pred. No. 4.3e-32;
ive 85; Mismatches 214; Indels
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A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
North W., Marra M.A.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                            :|| ::| | : | | : | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
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| : | : | | : | | : | | BASAVAÇGSQL-LVHSVDRWVNTTFICTATNAVGTGRAEQVILVRESP--STAGAGATGG 351
                                                                                                                            VIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL 423
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046770; ARH46770.1;
GD; GO:0005615; Pvr12.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; F:protein binding; IPI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Last annotation update)
2.
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STRAIN=C57BL/6; TISSUE=Brain;
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STRAIN=C57BL/6; TISSUE=Brain;
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Length 530;

19.8%; Score 537; DB 2; 28.6%; Pred. No. 7.3e-32;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 PQK--DLFQPEHLPLQTQF-------KEREVGNLQH------SNGLN----- 455
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US-09-778-510-2
US-08-665-531-1
US-08-665-531-1
US-08-966-531-1
US-08-966-531-1
US-09-96-945-2
US-09-570-367C-19
US-09-570-367C-19
US-09-949-016-6213
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US-09-949-016-6515
US-09-949-016-611044
US-09-949-016-611044
US-09-949-016-6115
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sequence 11380, Application US/09949016

patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOODI307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PASISEQ for Windows Version 4.0

LENGTH: 514
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7850, Ap
2, Appli
11044, A
6515, Ap
10054, A
5, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
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85; Mismatches 176;
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Matches 151; Conservative
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APPLICANT: Universita degli Studi di Bologna
APPLICANT: Universita degli Studi di Bologna
APPLICANT: Institut National de la Sante et de la Recherche M
TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
TITLE REPERBENCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
KUNMER OF SEO ID NOS: 2
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                                                                         403 -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDY
                                                                                                                       ----EKKAGPLGGS----SYEE
                                                                                                                                                                       EDENPVGEDGIQQM----YPLYN------QMCYQDRSPGKHHQNNDPKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GRNVSLKCLIE----VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
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PEATURE:
OTHER INFORMATION: Original Source: Hela Cell Line
OTHER INFORMATION: General Functional Class of Gene:
OTHER INFORMATION: Superfamily
OTHER INFORMATION: Binding Macromolecules: HSV-gD
OTHER INFORMATION: Subcellular localisation: Plasma NOTHER INFORMATION: Other Information: Viral Receptor
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                                                                                                                       401 SKAGIPOHH--PPMAQNLOYPDDSDÖ-
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Patent No. 6469155
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SEQ ID NO 1
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nes 137, Conservative
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                                                                                                                         --EKKAGPLGGS----SYEE 435
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                                                                         -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARNES, Morgyn S.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: COHEN, Gary H.
APPLICANT: WHITBECK, Charles J.
APPLICANT: RUMMENACHER, Claude
APPLICANT: RUMMENACHER, Claude
APPLICANT: WHITBECK, Charles J.
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APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBER: USOO,050/201
CURRENT FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                       EDENPVGEDGIQOM----YPLYN--------
                                                                                                     | | | : : | | SKAGIPQHH--PPMAQNLQYPDDSDD
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Patent No. 6641818
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SEQ ID NO 4
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Best Local S:
Matches 151
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Sequence 2, Application US/09723368
Patent No. 6641818
GENERAL INFORMATION:
APPLICANT: NORTHWESTERN UNIVERSITY
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WARNER, Morgyn S.
GERAGHTY, Robert G.
MARTINEZ, Wanda M.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.29
Best Local Similarity 30.39
Matches 131, Conservative
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FILLRVRRRRKS 436
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-----VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTQFKEREVGNLQHSN 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 YISDVPFKQTS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLD 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 NITEFPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVALRRRHTFKGDYST 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GNETVAAICIAATGKPVAHIDWE-------GDLGEMESTTTSFPNETATIISQYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.9%; Score 565.5; DB 4; Length 518; 29.0%; Pred. No. 1.6e-44; tive 85; Mismatches 171; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 GLNSRSFDYEDENPVGEDGIQQM----YPLYN----
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Y---DPEQLDLAENMVSQNDGSFISKKEWYV 518
                                                                                                                                                                                 APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS; FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 20
| : |: | | | | | : | 14
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Patent No. 6812339
                                                                                                          ; Sequence 20, Application US/09919172; Patent No. 6673545; GENERAL INFORMATION:
APPLICANT: Faris, Mary
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18; Conservative
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ORGANISM: Homo sapiens
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US-09-949-016-7563
                                                                                        -09-919-172-20
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Best Local S:
Matches 148
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7563

TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: ::|||::| ::||365 LENTTFVCTVTNAVGMGRAEQVIFVRETPRASPRDVGPLVWGAVGGTLLVLLLAGGSLA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 IIVEPHVTAVWGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFSVQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 VQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGPSFPS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 BYQG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 VSVTGYDGNWFVGRKGVNLKCNADANPPFFKSVWSRLDGQWPDGLLASDNTLHFVHPLTF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 NYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA--VAGAVIGAVLALFIIA--IFV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RPSPLCP-GGGKAQL-SSASLLGAGLLL---QPPTPPPLLLLLFPLLLFSRL-CGALAGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 RPPQSGPRASGRAQSPPGPSMARAALLPSRSPPTP----LLWPLLLLLLETGAQDVR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 465; DB 4; Length 52
30.3%; Pred. No. 5e-35;
ive 68; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONTGOMERY, Rebecca I.
COHEN, Gary H.
EISENBERG, Roselyn J.
WHITBECK, Charles J.
KRUMMENACHER, Claude
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APPLICANT:
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JS-09-949-016-6278
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Batent No. 6812303

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | | | : | | | | : | | HGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDP-----T 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDATLAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PPTP-----LLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL 67
                                                                                                                                                                                                                                                                                                                                                                                                                          33 PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI---EVNETITQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAAICIAATGKPVAHI------DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 2005/201
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR APPLICATION NUMBER: US. 60/087,862
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENT Ver. 2.1
SEQ ID NO 2
LENGTH: 479
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30.2%; Pred. No. 1.8e-34;
iive 66; Mismatches 160;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-8
NUMBER: FASTATION NUMBER: 60/231,498
NUMBER: FASTATION NUMBER: 60/231,498
SEQ ID NO 6278
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.29
Matches 121; Conservative
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-723-368-2
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ORGANISM: Human
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GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: Z000-04-14
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOCTUMENT OF SEQ ID NOS: 207012
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SOCTUMENT OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                   136 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGFDSLIDGGNET 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
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                                                                                                                                             33 PPTPPPLLLLLFPLLLFSRL-CGALAGPIIVEPHVTAVWGKNVSLKCLI----EVNETITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           189 VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ASLIGA-GLLLOPPTPPLLLLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 LIEVNET----ITQISWEKIHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDA
Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 456;
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Best Local Similarity 29.4%; Pred. No. 1.5e-29;
Matches 112; Conservative 68; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
16.9%; Score 458.5; DB 4; 30.2%; Pred. No. 1.8e-34; iive 66; Mismatches 160;
                                                                                                                                                                                                                     89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-7564; Application US/09949016; Patent No. 6812339
Query Match 16.9
Best Local Similarity 30.2
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 -----VAKCISANGHPPGRISWPSNVNGSHREMKE-PGSQPG-TTTVTSYLSMVPSRQAD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299
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                                                                                                                                                                                                                Sequence 62, Application US/09724864

Patent No. 6380362

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Watson, James D

APPLICANT: Watson, James G.

TITLE OF INVENTION: Polynuclectides and methods for their use.

TITLE OF INVENTION: Polynuclectides and methods for their use.

TITLE OF INVENTION: 1000.1050U1

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AQLARAT------RSPLSWLLLLF------CYALRKAGGDIRVLVPYNSTGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 KNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 GSTTLHCSLTSNENVTITQITWMKKDSGGSHALVAVFHPKKGPNIKEPERVKFLAAQQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 AQLSSASILGAGILLOPPTPPLILILIFPLILFSRLCGAL--AG---PIIVEPHVTAVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTGYDGNWFVGRKGVNLKCNADANPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%; Score 400.5; DB 3; Length 30.8%; Pred. No. 4.2e-29; Live 64; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 KPENMQQNTRLHLGYIFLIVFVLAVVIIIAALYTIRRCR 374
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CURRENT APPLICATION NUMBER: US/09/776,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/179
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
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; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
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Matches 123; Conservative
          387 TV 388
                                                                360 GI 361
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-724-864-62
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Patent No. 6812339

GENERAL INFORMATION:
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SLRMPGLRVEDEGNYTCLFVTFPQGSRSVDIWLRVLAKPONTAEVQKVQLT---GEPVP 230
                                                                                                                                               VKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRL 307
                                                                                                                                                                                                                                                                          351 MGPLPPFAVAQGAQL-LIRPVDKPINTTLICNVTNALGARQAELTVQVKEGPPSEHSGMS 409
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                                                                                                      AAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCV 247
                                                                                                                                                                                                                                                                                                                                                               DGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 VAGAVIGAVLALFIIAIFVTV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : : | : : 410 -RNAIIFLVLGILVFLILLGI 429
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Best Local Similarity 29.3'
Matches 106; Conservative
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ORGANISM: Human
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US-09-949-016-6729
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                                                                                                                  104 SSELKVSLITNVSISDEGRYFCQLYIDP--PQESYTTITVLVPPRNLMIDIQKDTAVEG-- 159
                                                                                                                                                                                                                                                                  215 GVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
                                                                                                                                                                                                                                                                                                                                          275 PVMVTWVRVDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDP 333
                                                                                                                                                                                                                                                                                                                                                                                                                64 PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF 123
                 127
                                                                                                                                                                   ETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                          ------KQTSSIAVAGAVIGAVLALFIIAIFVTVL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : ::|: | | : SVVLPSGSQCAAAAAA------AAPPGLRLL---LLLFS--AAALIPTGDGQNLFT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PT 109/9866,028
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALA----GPIIVE
                                        54 VIEGEVATISC--QVNKSDDSVI--QLINPNRQTI-----YFRDFRPLKDSRFQLINFS
                                                                                                                                                                                                                                           241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPP
                 68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                         128 INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGN
                                                                                                                                                                                                                                                                                                                     299 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDV
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                                                                                                                                                                                                                                                                                                                                                                                               359 PF-----
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Filvaroff, Ellen
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Matches 108; Conservative
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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Roy, Margaret
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APPLICANT:
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Patent No. 6556493
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, Roger
APPLICANT: REEVES, ROGER
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT PELLING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                              54 VIEGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLNFF 103
                                                                                                                                                                                                                                                                                                                                                                                               LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KQTSSIAVAGAVIGAVLALFIIAIFVTVL 389
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                                                                                                                                                                                                                                             8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVT
                                                                                                                                                                                                                                                                                  3 SVVLPSGSQCAAAAAAAAPPGLRLR-----LLLLLFSA---AALIPTGDGQNLFTKDVT
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                                                                                                                                                                   Length 442;
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                                                                                                                                                                   cch 11.3%; Score 306.5; DB 4; al Similarity 25.0%; Pred. No. 3.7e-20; 106; Conservative 78; Mismatches 173;
1998-08-07
                   NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
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                                 SOFTWARE: Patentin V. SEQ ID NO 20
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapien
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ORGANISM: Homo sapiens
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 106; Conserv
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Matches 106; Conserv
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                                                                                                                                US-09-778-510-20
   PRIOR FILING
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US-09-930-803-1
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ORGANISM: Homo Sapien
US-09-944-457-61
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Best Local Simi
Matches 108;
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                                                                    124 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLI 182
                                                                                                   98 LNFSSSELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAV 155
                                                                                                                                                                                        209 KEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAI 268
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                                                                                                                                                                                                                                                                                                                                          295 ANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIY 354
48 KDVTVIEGEVATISC--QUNKSDDSVI--QLINDNRQTI-----YFRDFRPLKDSRFQL 97
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TITUS OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
                                                                                                                                                         DGGNETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSPPNETATIISQYKLFPT
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-26
PRIOR PLILING DATE: 2001-05-26
PRIOR PLILING DATE: DOCEMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 11, 1997
PRIOR PLILING DATE: DECEMBER 16, 1997
PRIOR PLILING DATE: DECEMBER 16, 1997
PRIOR PLILING DATE: DECEMBER 16, 1997
PRIOR PLILING DATE: DECEMBER 16, 1997
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APPLICATION NUMBER: 60/069,702
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Patent No. 6734288
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Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
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Botstein, David
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Goddard, Audrey
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Tumas, Daniel
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 APEVSVTGYDGNWFVGRKG--VNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFV 325
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                                                                                                                      DGGNETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETATIISQYKLFPT 236
                                                                                                                                          :| | : | | : | | | | | | | EG--EEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMY-----TVTSQLMLKVH 208
                                                                                                                                                                                                                                                                                                                             -----KQTSSIAVAGAVIGAVLALFIIAIF 385
                                                                                                                                                                                                                                                                                                                                                95 HGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PQESYTTITVLVPPRNLMIDIQKDTAVEG--EEIEVNCTAMASKPATTIRWFKGNKEL 168
                                                                                                                                                                                          RFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNAD 294
                                                                                                                                                                                                                                                           ANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIY 354
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48 KDVTVIEGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRPQL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 PPPL-LLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daum, Peter
From: Molecules Designated B7L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQUENCE 222, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT PILING DATE: 2001-02-07
FRIOR APPLICATION NUMBER: 66/095,663
FRIOR APPLICATION NUMBER: 66/095,663
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1998-08-07
SCOFTWARE OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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1999-08-05
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ORGANISM: Mus musculus
US-09-778-510-22
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Search completed: October 6, 2005, 09:44:24 Job time : 23.3581 secs

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Sequence 12, App. Sequence 10, App.
                                                                           October 6, 2005, 09:13:38; Search time 237.135 Seconds (without alignments) 894.712 Million cell updates/sec
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Sequence 18,
Sequence 31,
Sequence 6, A
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1 MARTLRPSPLCPGGGKAQLS......KHHQNNDPKRVYIDPREHYV 510
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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-972-268-8
US-09-959-845-4
US-09-972-268-18
US-09-972-268-18
US-09-972-268-19
US-09-972-268-19
US-09-972-268-6
US-10-161-572-268-6
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Maximum DB seq length: 2000000000
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Sequence 16, Appl	4	ď	13	15,	ď	17,	60,	20,	21,	20,	e 20,	147	Sequence 15, Appl	33,	114	116	12	37	39	'n	33	23	13	138	61	17	17	25	36			Sequence 66, Appl	16
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ALIGNMENTS

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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy B.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE OF INVENTION: NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR APPLICATION NUMBER: 39
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 39
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                 ; Sequence 12, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: homo sapiens
US-09-972-268-12
US-09-972-268-12
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Sequence Sequence

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APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Soremsen, Eatc A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKI
FILE REFERENCE: 3101-A
CURRENT APPLICANTION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-10-05
PRIOR PRIOR PLILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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                                          181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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Publication No. US20030044893A1
GENERAL INFORMATION:
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TYPE: PRT

CRGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Soronsen, Exic A.
APPLICANT: Soronsen, Exic A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE PITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE OURSENT APPLICATION NUMBER: US/09/972,268
CURRENT APPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
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IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                    VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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Pred. No. 8.8e-197;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QMCYQDRSPGKHHQNNDPKRVYIDPREHYV 510
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; Publication No. US20030044893A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6%;
Matches 508; Conservative
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US-09-972-268-10
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LENGTH: 510
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; Sequence 18, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
    APPLICANT: Baum, Peter R.
    APPLICANT: Baum, Peter R.
    APPLICANT: Baum, Exter R.
    APPLICANT: Sociensen, Milliam C.
    APPLICANT: Sociensen, Exter A.
    APPLICANT: Youakim, Adel
    TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF MAKING AND USE TITLE OF INVENTION: NUMBER: US/09/972,268
    CURRENT APPLICATION NUMBER: US/09/972,268
    CURRENT FILING DATE: 2000-10-05
    PRIOR APPLICATION NUMBER: 60/238,557
    PRIOR APPLICATION NUMBER: 60/238,557
    NUMBER OF SEQ ID NOS: 39
    SOFTWARE: Patentin version 3.1
    SES ID NO 18
    SES ID NO 18
    SES ID NO 18
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88.8%; Pred. No. 1.6e-173;
iive 22; Mismatches 33;
                                                                                                          NOMCYQDRSPGKHHQNNDPKRVYIDPREHYV 510
                                                                                                                               Query Match
Best Local Similarity 88.8%
Matches 454; Conservative
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241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
                                  IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                        AVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYBERSPPLPQK 426
                                                                                                                                                                 DLFQPEHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQMCYQD 486
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09959845
Publication No. US20030008334A1
GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Kesiko SATO
APPLICANT: Kenichi TAKAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-16784AC/00653
CURRENT PELLING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-065595
PRIOR PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 4
                                                                                                                                                                                                                                           RSPGKHHQNNDPKRVYIDPREHYV 510
                                                                                                                                                                                                                                                                Matches 454; Conservative
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; ORGANISM: Mouse
US-09-959-845-4
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Sequence 19, Application US/09912268

Publication No. US20030044893A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Lofton, Timothy B.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Sorensen, Seic A.

APPLICANT: Octable Sorensen, Sorensen, Seic A.

APPLICANT: Sorensen, Sorensen, Seic A.

APPLICANT: Octable Sorensen, Seic A.

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APPLICANT: Sorensen, Seic A.

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APPLICANT: Sorensen, Seic A.

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                 FILE REFERENCE: 2001-1678A/LC/00633
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
FRIOR PILING DATE: 2001-03-09
FRIOR APPLICATION NUMBER: PCT/JP01/01871
FRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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US-09-972-268-19
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                                                                                                                        Sequence 31, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Coffcon, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE:
TITLE REFERENCE: 3101-A
CURRENT FILIG DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
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481 SOMCHODRSPROHHPRN-PERLYINPREHYV
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Publication No. US20030008334A1
GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyaki NAKANISHI
APPLICANT: Keiko SATO
APPLICANT: Kenichi TAXAHASHI
APPLICANT: Kenichi TAXAHASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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ORGANISM: homo sapiens
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US-09-972-268-31
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US-09-959-845-6
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Publication No. US20030044893A1

GENERAL INPORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Fanelow, William C.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Youakim, Adel

TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE 7

FILE REPRENCE: 3101-A

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/238,557

PRIOR APPLICATION NUMBER: 60/238,557

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1
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                                                                                      Length 438;
                                                                                    Query Match 77.8%; Score 2107; DB 10; Length Best Local Similarity 93.2%; Pred. No. 3.7e-152; Matches 399; Conservative 12; Mismatches 17; Indels
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61 IVEPHVTAVWGKAVSLKCLIEVNETI 61 IVEPHVTAVWGKAVSLKCLIEVNETI 121 VLFKAVSLNDATITLHNIGFSDSGKY 121 VLFKAVSLNDATITLHNIGFSDSGKY 181 LIDGGNETVAAICIAATGKPVAHIDM 181 LIDGGNETVAAICIAATGKPVAHIDM 241 GRRITCVVKHPALEKDIRYSFILDIG 241 GRRITCVVKHPALEKDIRYSFILDIG 241 GRRITCVVKHPALEKDIRYSFILDIG 301 KSVWSRLDGGWPDGLLASDNTLHFVH 360	y OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc US-09-972-268-14 Query Match Query Matches 373; Conservative 3; Mismatches 18; Indels 38; Gaps 2; Matches 373; Conservative 3; Mismatches 18; Indels 38; Gaps 2; Qy MARTIREPSPLCPGGGRAQLSSALLGAGILLQPPPPPLLLLEFPLLLFSRLCGALAGPI 60 Db MARTPGPSPLCPGGGRAQLSSALLGAGILLQPPPPPPLLLLFPLLLFSRLCGALAGPI 60 Qy G IVEPHVTAVWGRAVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120

6 6 6 6 6	241 GRRITCCVCKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300 241 GRRITCCVCKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFRYSGVYICKVTNSLGQRSDQKVIYISDVPF 360	8 8 8 8	:
RESULT 108-09-69-69-69-69-69-69-69-69-69-69-69-69-69	SULT 13 Sequence 4, Application US/09972268 Sequence 4, Application US/09972268 Publication No. US20030044893A1 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Enablow, William C. APPLICANT: Lofton, Timothy E. APPLICANT: Sorensen, Eric A. APPLICANT: Sorensen, Aci TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A TITLE OF INVENTION NUMBER: 0S/09/972,268 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 60/238,557 PRIOR APPLICATION NUMBER: 60/238,557 NUMBER OF SEQ ID NOS: 39 SOFTWARE: PatentIn version 3.1 LENGTH: 549 TYPE: PRT ORGANISM: Artificial Sequence	RESULT 14 US-09-972 Sequency GENERALS APPLIC	SULT 14 1-09-972-268-2 2-269-2 2-264-2 3-201-20-3-2-268-2 3-201-20-3-2-268-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3
CO CO	FEATURE INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fro OTHER INFORMATION: m human Nectin-3 alpha -09-972-268-4	Query Match Best Local Matches 38	y Match Local Similarity 67.5%; Pred. No. 3.9e-135; hes 383; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
Quer Best Matcl	Query Match Best Local Similarity 67.6%; Pred. No. 1e-136; Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;	oy B	8 SPLCPGGGKAQLSSASLLGAGLLLQPPPPPLLLLFPFLLFSRLCGALAGPIIVEBHVT 67
λ Β	1 MARTIRPSPICPGGGKAQLSSASLIGAGLILQPPTPPPLILLIFPLILFSRLCGALAGPI 60	ò a	68 AVWGKNVSLKCLIEVNETITOISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYS 127
, 6 Q	61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120 	oy Og	128 LNDATITLHNIGFSDSGXXICKAVTFPLGNAQSSTTVTVLVEFTVSLIKGFDSLIDGGNE 187
ر م	121 VLFRUYSLNDATITLHNIGFSDSGKYICKAVFFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 	ç q	188 TVAAICIAATGKPVAHIDWEGDLGEWESTTTSFPNETATIISQYKLPPTRFARGRRITCV 247
λ β	181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATHISQYKLFPTRFAR 240 	oy qa	248 VKHPALEKDIRXSFILDIQYAPEVSVTGYDGNWFVGRKGYNLKCNADANPEPFKSVWSRL 307
ъ д В	241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPF 300 	λό O	308 DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP 359
& a	301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVXICKVTNSLGQRSDQKVIXISDVP- 359 	oy op	360
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δ	384 IFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERSPPLP 424	ò	432 EHLPLQTQFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYPLYNQMCYQDRSP 489

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Sequence 13, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Loftcon, Timothy E.

APPLICANT: Loftcon, Timothy E.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

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APPLICANT: Sorensen, Eric A.

SORTHARE: Patentin version 3.1

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69.7%; Score 1885.5; DB 10; Length 634;
Best Local Similarity 83.9%; Pred. No. 4.8e-135;
Matches 371; Conservative 7; Mismatches 45; Indels 19;
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FC
US-09-972-268-13
                                                                                       490 GKHHQNNDPKRV-----YIDPREHYV 510
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Copyright (c) 1993 - 2005 Compugen Ltd
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asthma, allergy, allograft rejection, metastasis of cancer cells, the kidner transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogeneic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3gamma protein.
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Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

Claim 1; Page 98-99; 141pp; English

sepsis, stroke.

Youakim A;

Sorensen EA,

Lofton TE,

Fanslow WC,

Baum PR,

2002-426103/45.

N-PSDB; AAD37445

05-OCT-2000; 2000US-0238557P 05-OCT-2001; 2001WO-US031392

(IMMV) IMMUNEX CORP

/note= "Intracellular C-terminal domain"

WO200228902-A2

11-APR-2002

domain"

/note= "Extracellular Ig

'note=

Modified-site

189.

Domain

/note= "Extracellular Ig /note= "N-glycosylated" 386. .510

"N-glycosylated"

'note=

Modified-site

287

Domain

Modified-site

Domain

domain"

"Extracellular Ig

"N-glycosylated" 'note= "N-glycosylated" "N-glycosylated"

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The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polymucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adeneral junction formation activity, epithelial corresponding bring a ctivity, rital polypeptide binding activity. The epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The above mentioned method is inflammation, sepsis, cedema, diabetic retinopathy, asthma, allery, allograft rejection, metastasis of cancer cells, parcellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, inhibiting angiogenesis in a mammal and traisme or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restences a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restences a subject, such as ischaemia and treating herpesvirus infection.
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Human nectin-3beta protein.

FILLEX

Key Modified-site Homo sapiens

Domain

(first entry)

27-AUG-2002 AAE23286;

AAE23286

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Gaps .; 0

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                                                                                                                                                                Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
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The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Section by and protein are useful for treating a disease associated with cell adhesion activity, adherens juuction formation activity, epithelial cell adhesion activity, ral polypeptide binding activity, epithelial or migration activity, ral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, catcher cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for the kidney or inflammatory bowel disease. Nectin DNA is also useful for condition of a tissue or a subject, such as isochaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenorsis, tumour growth and treating herpesvirus infection.

C Nectin is also useful for modulating proliferation or migration of an endothelial cell). The present sequence is a fusion protein encoding 6 amino actids from mouse nectin-3 protein and the rest form human nectin-3 beta agene is located on chromosome 3.

C Updated on 29-AUG-2003 to standardise OS field)
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Pred. No. 8e-176;
0; Mismatches 2; Indels (
Claim 1; Page 94-95; 141pp; English.
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Best Local Similarity 99.5
Matches 428; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 510 AA;
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361 AVAGAVIGAVLALFIIAIFVTVLLIPRKKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK 420

DLFQ 430 DLFQ 424

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367 AVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK

366

306 300

241 VVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSR

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VVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSR

301 LDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSI

307 LDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSI

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gamma and nectin-4 polypeptides and their corresponding polymolecides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenests in a mammal and treating endothelial migration, inhibiting angiogenests in a mammal and treating endothelial migration, is considered in a subject, such as stroke, restenosis, tumour growth and treating herpeavirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-section.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, for treating or preventing heart failure, malaria,
Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allorgy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosolerosis; isolaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a substantially purified nectin3alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
                                                                                                                                                                                                                                                                                                                                                                                          Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                          Sorensen EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3beta gene is located on chromosome 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 89-91; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Lofton TE,
                                                                                                                                                                                                                                                                                                    05-OCT-2000; 2000US-0238557P
                                                                                                                                                                                                                                                            05-OCT-2001; 2001WO-US031392
                                                                                                                                                                                                                                                                                                                                                                                          Baum PR, Fanslow WC,
                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
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                                                                                                                                                                          40200228902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis, stroke
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                    11-APR-2002
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Best Local S
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| IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                                                                                     cell adhesion; cell infiltration; cancer metastasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and
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                                                                                                                                                                                                                                                                                                                                                                                   Sato
                                                                                                                          of murine nectin-3.
                                                                                                                                                                                                                                                                                                                                                                                   Nakanishi H,
                                                                                                                                                                                                                                                                                                                                & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 45-48; 64pp; Japanese
                              AAG63983 standard; protein; 510 AA.
                                                                                                                                                                                                                                                                            09-MAR-2001; 2001WO-JP001871
                                                                                                                                                                                                                                                                                                          09-MAR-2000; 2000JP-00065595
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corresponding antibodies.
                                                                                                                                                                                                                                                                                                                                                                                   rakahashi K, Takai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2001-570771/64.
                                                                                                                        Amino acid sequence
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TAKAHASHI
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH78180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 510 AA;
                                                                                                                                                                                                                 WO200166736-A1.
                                                                                          26-NOV-2001
                                                                                                                                                                                                                                            13-SEP-2001
                                                                                                                                                     Nectin-3;
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Pred. No. 1.1e-174;
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100.0%; Pred. No. 1...
... 0; Mismatches
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IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR 120
                                                                                                                                                                                                 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                 KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNXSGVYVCKVSNSLGQRSDQKV1YISDIPL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischamma-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma.
                                                                                      VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                     VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                                                                                                                                                  GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema
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mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, as albograft rejection, metastasis of cancer cells, paracellular transport disorders such as wich as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is mouse nectin-3beta protein
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                                                                                                                                                                                                                91.7%; Score 2108; DB 5; 92.2%; Pred. No. 1.1e-164;
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Matches 400; Conserv
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The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mentioned method is inflammation, sepals, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is mouse nectin-3gamma protein
      metastasis; restenosis; inflammatory bowel disease;
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           allograft rejection; metastasis; restenosis; inflammatory bowel di
oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
stroke; tumour; cancer; herpesvirus infection; asthma.
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                                                                                                                                                                                                                                                                                                                                                       Youakim A;
                                                                                                                                                                                                                                                                                                                                                         Sorensen EA,
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                                                                                                                                                                                                                                                                                                                                                       Lofton TE,
                                                                                                                                                                                                                           05-OCT-2001; 2001WO-US031392
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Matches 399; Conservative
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                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sepsis, stroke
                                                                                                                                         WO200228902-A2
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                                                                                                                                                                                                                                                                                                                                                     Baum PR,
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                                                                                                                                                                                                                                                                                                           The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGFDS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                 or diagnosing and treating tumor infiltration and the mouse nectin-3 protein families and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%; Score 2107; DB 4; Length 438; 93.2%; Pred. No. 1e-164; Live 12; Mismatches 17; Indels
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                                                                               Sato
                                                                           Nakanishi H,
& TECHNOLOGY CORP.
K.
                                                                                                                                                                                                                                                                       Claim 3; Page 53-55; 64pp; Japanese
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Matches 399; Conservative
                                                                                                                                                                                                                             corresponding antibodies.
                                                                           Takahashi K, Takai Y,
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                                                                                                                     WPI; 2001-570771/64
                                                                                                                                                                                   protein family
             JAPAN SCI
TAKAHASHI
                                                                                                                                           N-PSDB; AAH78181
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                                                                                                                                                                                                           metastasis
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                                             TQTSSIAVAGAVIGAVLALFIITVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYEERI 420
            KSVWSRLDGOWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGORSDOKVIYISDIPL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to nectin-1,
                                                                                                                                                                                                                                               Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischamia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
                                  KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS
Novel purified nectin-3 and nectin-4 polypeptides which bind to nect
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Youakim
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/note= "FLAG peptide"
382. .387
/note= "PolyHis tag"
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                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Unidentified.
Chimeric.
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                      ischaemia, atheroscierosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3beta-FIAGpolyHis fusion protein
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tissue or a subject,
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                                                                                                                                                                                                                                                                    83.2%; Score 1912; DB 5; Length 387; 99.5%; Pred. No. 1e-148; ive 0; Mismatches 2; Indels C
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angiogenic condition of a
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Best Local Similarity 99.5
Matches 363; Conservative
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                                                                                                                                                                                                                   Sequence 387 AA;
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Chimeric.
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27-AUG-2002 (first entry)

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                                                                                                                                                                                                                                                                                    The invention relates to a substantially purified nectinialpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above
                                                                                                                  Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing human nectin-3beta protein fused to immunoglobulin 1gg1 Fc region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer calls, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
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                        Sorensen EA, Youakim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.8e-148;
0; Mismatches 2;
                                                                                                                                                                                                                                          9; Page 102-104; 141pp; English.
                        Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.2%;
99.5%;
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Best Local Similarity 99.5
Matches 363; Conservative
                        Fanslow WC,
                                                                        WPI; 2002-426103/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 595 AA;
                                                                                                                                                                                               sepsis, stroke
                        Baum PR,
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                                                                                                                                                                                                                                                           GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300
                                                                                                                                                                                                                                                                                       GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                              LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                       MARTPGPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLLFPLLLFSRLCGALAGPI
                                                               IVEPHVTAVWGKNVSLKCLIEVNETITOISWEKIHGKSSOTVAVHHPOYGFSVOGEYOGR
                                                                                               IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                             VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
                                                                                                                                                                                           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISOYKLFPTRFAR
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AAE23283 standard; protein; 549 AA.

AAE23283

RESULT 11
AAE23283
ID AAE23
XX
AC AAE23

The epithelial or

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gamma and nectin-4 polypeptides and their corresponding polynuclectides.

Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, parcellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, condition or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
                                                             nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
                                                                          paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metaetasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischemmia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a substantially purified nectin3alpha, beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Youakim A;
                                                                                                                                                                                                                                                        'note= "Extracellular Ig domain"
                                                                                                                                                                                                                                                                                                                                                                                        domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                           'note= "Extracellular Ig
                                                                                                                                                                                                                        /note= "N-glycosylated"
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                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lofton TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2001; 2001WO-US031392
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                               protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
                               Human nectin-3alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-426103/45.
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                                                               Human;
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02-DEC-2004
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ADR66369
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AC ADR66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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                                                                                                                                                                                                                                                                            1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPFLLEFSRLCGALAGPI
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Nectin is also useful for modulating proliferation or migration of an endethelial cell, an epithelial cell or a smooth muscle cell (vascula smooth muscle cell). The present sequence is human nectin-Jalpha DNA. Human nectin-Jalpha gene is located on chromosome 3
                                                                                                                                                                                                       49;
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                                                                                                                                                          Length 549;
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                                                                                                                                                        ; Score 1902.5; DB 5; Length
; Pred. No. 9.7e-148;
16; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related protein
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10-OCT-2001; 2001US-0328655P.
22-OCT-2001; 2001US-0333P.
15-FEB-2002; 2002US-0357539P.
15-FEB-2002; 2002US-0357600P.
                                                                                                                                                            82.8%;
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                     Query Match
Best Local Similarity
Matches 372; Conserv
                                                                                                                  Sequence 549 AA;
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ABJ20222
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The invention relates to a novel method for identifying a candidate p53 pathway modulating agent. The method comprises providing an assay system having a purified IG polypeptide or nucleic acid, or their functionally active fragment or derivative. The method is useful for identifying modulators of the p53 pathway, particularly for identifying agents for treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung cancer or cancer of the ovary) associated with defective p53 function.

The identified modulators are useful as targets for novel therapeutics. The identifiers of the p53 pathway, and as therapeutic rargets for novel therapeutics. The method is also useful for diagnosing disorders associated with defective p53 pathway, and as therapeutic targets for disorders associated with defective p53 function. This sequence represents a human protein relating to the human IG genes used in the assay for identifying modulators of the p53 pathway of the invention
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                                                                                                                    Identifying a candidate p53 pathway modulators that are useful as targets for therapeutics or for diagnosing cancers associated with defective p53 function, by providing an assay system having a purified IG polypeptide
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  Francis-Lang
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                                                                                                                                                                                                                                                 Claim 13; Page 206-209; 248pp; English
  Belvin M,
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  Plowman GD,
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Best Local Simi:
Matches 372;
                            Lioubin MN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosins is based on cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, container interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the colypeptide, preferably humanised or human; an anti-idotype, non-human container are group, cell toxin, immunostimulatory molecules and/or with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concertially with anti-human CD4 murine monoclonal antibodies; bicinylated second antibody; streptavidin-conjugated horseradish concertially but non-malignant cells only weakly. In 15 of 51 samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples were also stained. ADR65054 represent the conversioned and cytoplasmic staining was very strongy invention.
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Bruemmendorf T, Kinnemann H, Roepcke S;
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#2.
  prostatic carcinoma derived protein SEQ ID 223
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                                                   human; cytostatic; diagnosis; prostatic cancer; differential expression analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 703; 1607pp; German.
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14-MAY-2003; 2003DE-01022134.
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Best Local Similarity 79.33
Matches 372; Conservative
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ROSENTHAL A.
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                                                                                                                                            Homo sapiens
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361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
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3, Bruemmendorf T, Kinnemann H, Roepcke S;
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                                                                                                                                121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEVEPTVSLIKGPDS
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                                                  61 IVEPHVTAVWGKNVSLKCLIBVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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                                                                                                                                                                         181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
                                                                                                                                                                                                                                     241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                                                                                                                                                                   KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP-
                                                                                                                                                                                                                                                                                                                                                                                                                             384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostatic carcinoma derived protein SEQ ID 223 #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; cytostatic; diagnosis; prostatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 1205; 1607pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differential expression analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR66711 standard; protein; 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2003; 2003DE-01009985.
14-MAY-2003; 2003DE-01022134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2004; 2004WO-DE000433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beckmann G,
Staub E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinzmann B, Dahl E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-653386/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004076614-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agents.
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4.

Gaps

49;

32; Indels

AAE23282 standard; protein; 549 AA.

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody directed against an anti-idiotype, non-human (monoclonal) antibody directed against an anti-idiotype, non-human (monoclonal) antibody directed against an anti-idiotype, non-human (monoclonal) antibody directed against an anti-idiotype, non-human (monoclonal) antibody directed against an anti-idiotype, non-human (monoclonal) antibody directed against an or any of the above darivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that prostatic cancer patients, or subjects at risk, were incubated concerned antibody, streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The sequentially with anti-human CDH murine monoclonal antibodies; supplementationally with non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention

Sequence 549 AA;

61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120 61 IVEPHYTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQIVAVHHPQYGFSVQGEYQGR 120 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFF 300 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359 -----FKQTSSIAVAGAVLALFIIA 383 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI 60 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI Gaps 49; DB 8; Length 549; 32; Indels 82.8%; Score 1902.5; DB 8; 79.3%; Pred. No. 9.7e-148; ive 16; Mismatches 32; Matches 372; Conservative Local Similarity 360 301 121 121 181 181 241 241 301 Query Match g 임 g a ద à 셤 ò ò ò ò ద ⋧ ò

Human, nectin-Jalpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein; Youakim /note= "Human nectin-3alpha protein" Mouse nectin-3-human nectin 3alpha fusion protein. Sorensen EA, 1. .7 /note= "Mouse nectin-3 protein" Location/Qualifiers Lofton TE, 05-OCT-2001; 2001WO-US031392 05-OCT-2000; 2000US-0238557P (revised)
(first entry) . 549 Fanslow WC, (IMMV) IMMUNEX CORP WPI; 2002-426103/45. WO200228902-A2 Homo sapiens. Mus musculus. chromosome 3 29-AUG-2003 27-AUG-2002 11-APR-2002 PR, AAE23282; Chimeric. Key Region Region Baum

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Section DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial corresponding barrier function detrivity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, asthma, allergy, allograft rejection, metastasis of cancer cells, continuation of inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as isolatenal actions, thrombosi Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, Claim 1; Page 80-82; 141pp; English. sepsis, stroke.

N-PSDB; AAD37441.

Sequence 549 AA;

standardise OS field)

361 TTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420

384 IFVIVILIPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430

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RESULT 15 AAE23282

Query Match

5; Length 549; 08 82.1%; Score 1888.5;

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4,	09	09	120	120	180	180	240	240	300	300	359	360	383	420		
Gaps	ALAGPI	ALAGPI	GEYOGR	GEYQGR	IKGPDS	IKGPDS	PTRFAR	PTRFAR	ANPPPF	ANPPPF	TSDVP-	ISDPPT	ALFIIA	FIVLVS		
49;	FSRLCC	FSRLCC	YGFSVC	YGFSVC	EPTVSI	EPTVSI	SOYKLE	SQYKLE	LKCNAL	LKCNAL	DOKVI	DOKVI	VIGAVI	VVGGAI	0 430	Q 459
Indels	MARTIERPS PLC PGGGGKAQLSSAS LLGAGLLLQPPTPPPLLLLLEPPLLLES RLCGALAGP	MARTPGPSPLCPGGGKAQLSSASLLGAGILLLQPPTPPPLILLLFPULLFSRLCGALAGPI	I VEPHVTAVWGKAVVSLKCLI EVNETI TQI SWEKI HGKSSQTVAVHHPQYGFSVQGEYQGR		VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS		LIDGGNETVAAI CIAATGKPVAHI DWEGDLGEMESTTTSFPNETATI I SQYKLFPTRFAR	LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR	GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPF	GRRITCVVKHPALEKDIRXSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF	KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP	KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT	FKQTSSIAVAGAVIGAVLALFIIA	TTTLQPTIQMHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS	IFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ	OIDOLO
1.4e-146; hes 34;	TPPPLLI	TPPPLLI	HGKSSQ1	HGKSSQT	LGNAQS	LGNAOSS	STTTSF	STTTSF	GYDGNWE	GYDGNWE	VYICKV	VYICKV	FKQTS	ATIKOD	YEERSPI	HOKES-
d. No. 1.4e Mismatches	BLLLOPP	GILLOPP	DISWEKI	JISWEKI 2	CKAVTFP	KAVTEP	SDLGEME	SDLGEME	APEVSVI	APEVSVI	CIFNYSG	TENYSG	1 1 1 1 1	PFPLSTL	THKPPPL	: : NYIPPSDMQKES-
r L	ASLLGA	ASLLGA(VNETIT	VNETIT	DSGKY I	DSGKYI(AHIDWE	AHIDWE	ILDIQY	ILDIQY!	LHEVHP	LHEVHP]		TEPKKLI	VIDLPP	-
9%; 16	KAQLSS	KAQLSS	LKCLIE	LKCLIE	HNIGES	HNIGES	ATGKPV	ATGKPV	DIRYSE	DIRYSF	LASDNT	LASDNT	1	DIEDLA	PSYLDK	: :
vat	PLCPGGG	PLCPGG	WGKNVS	WGKNVS	NDATITI	MDATITI	AAICIA	AAICIA	CHPALER	H	SOWPDGI	3QWPDGI		WHPST?	PRKKF	: : RRRTFF
Similarity 10; Conser	TLRPS	TPGPSE	SPHVTA	SPHVTA	KUNYSLA	KONYSEN	GGNET	GGNET	LITCON	LITCON	WSRLDC	WSRLDC		rlopti(TVLLT	: AGIFCYF
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                    Copyright
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; Search time 14.3671 Seconds (without alignments) 2926.593 Million cell updates/sec US-09-972-268-31 6 Run

1 MARTLRPSPLCPGGGKAQLS......ERSPPLPQKDLFQVCVHEYT 437 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
3: pir2:*
1: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	poliovirus recepto			poliovirus recepto		poliovirus recepto	poliovirus recepto	poliovirus recepto	poliovirus recepto		irregular chiasm C	perlecan precursor	hypothetical prote	hemicentin precurs	OX-2 membrane glyc	adhesion molecule	surface glycoprote	neural cell adhesi	myelin-associated	myelin-associated	elastic titin - hu	myelin-associated	myelin-associated	Down syndrome cell	heparan sulfate pr	glial cell membran	coxsackie- and ade	B-cell adhesion pr
SUMMARIES	ΩI	T08732	JC4024	A53437	168093	HLMSP3	153960	B44194	A44194	RWHUPD	RWHUPA	A54017	A49448	A38096	T20992	T43290	A47639	JH0506	A45254	IJBONC	A61084	B33785	I38346	BNRT3S	BNRT3	T08851	\$18252	A58532	JC7780	JH0371
	82	7	7	N		Н	N	~	~		Н	N	~	7	~	~	~	~	~	-	1	7	~	Н		~	~	~	N	7
	Length	407	518	530	538	467	478	392	417	392	417	416	764	4391	5175	5198	274	588	588	853	626	637	7962	582	626	1896	3707	1091	365	847
do	Query Match	50.4	23.7	21.6	21.3	20.3	19.8	18.2	18.2	17.5	17.5	14.2	10.0	8.9	8.5	8.5	8.2	7.7	7.7	7.7	7.7	7.7	7.7	7.6		7.6	7.5	7.4	7.4	7.2
	Score	1159.5	544	495.5	490	467	455	418	418	402	402	326.5	229.5	205.5	196.5	196.5	187.5	178	178	177.5	177	177	176	175	175	174.5	173.5	171	170.5	164.5
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OX-2 membrane glyc	neural cell adhesi	DM-GRASP precursor	neural cell adhesi	cell adhesion mole	cell adhesion mole	cell adhesion mole	carcinoembryonic a	vascular cell adhe	neural cell adhesi	cell surface glyco	SHP substrate-1 pr	dutt1 protein - mo	neural cell adhesi	neural cell adhesi	kinase-like protei
TDRTOX	IJRTNC	JH0464	IJHUNG	C42632	B42632	A42632	A36319	JN0581	IJCHNL	I38049	JC5288	T30805	IJMSNG	IJMSNL	A39712
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278	828	587	761	765	812	932	702	739	1091	646	509	1612	725	1115	1051
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162.5 7.:							160.5								

ALIGNMENTS

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REST	

hypothetical protein DKFZp566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08732
R;Ottenwealder, B.; Dermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
B;Cetrence to the Protein Sequence Database, May 1999
A;Reference number: 216474
A;Accession: T08732
A;Accession: T08732
A;Accession: T08732
A;Accession: T08732
A;Accession: T08732

A;Cross-references: UNIPROT:Q9Y412; EMBL:AL050071
A;Experimental source: fetal Kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Gaps 49; Length 407; 32; Indels 50.4%; Score 1159.5; DB 2; 70.3%; Pred. No. 1.1e-77; ive 16; Mismatches 32; Query Match
Best Local Similarity 70.33
Matches 230; Conservative 143 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKFVA 202 203 HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 262 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA 60 셤 ò 8

323 HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP------121 셤 ઠે

359

241 EPKKLPPPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRFFRGDYFAK- 299 ------FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDKV 403 360 셤 q à

404 IDLPPTHKPPPLYEERSPPLPQKDLFQ 430 ----NYIPPSDMQKES----QIDVLQ 317

ઠે 셤

JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024

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251

234

294

423 411

351

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C;Accession: 168093

R;Eberle, F.; Dubreull, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
A;Eberle, F.; Dubreull, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR),
A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Accession: 168093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-538 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 OVTWORLDG---TVVAAFHPSFGVDFPNSOFSKDRLSFVRARPETNADLRDATLAFRGLR 122
                                                                                                                                                                                                                                                              140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGA 371
6 VLPPSRLSPTLPLLPLLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNIGFSDSGKYICKAVTPPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNET
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                                                                                                               88 QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG
                                                                                                                                                                                                                                                                                                                                    123 VEDEGNÝTČEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPQSV-----AVARČV
                                                                                                                                                                                                                                                                                                                                                                                                                 195 AATGKPVAHIDWEGDLGEMESTTTSPPN---ETATIISQYKLPPTRFARGRRITCVVKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 VIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | | | : | | | : | | HQLIVEDEGNYTCEFAIFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDP
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C;Superfamily: poliovírus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.3%; Score 490; DB 2; Lularity 29.3%; Pred. No. 2.6e-28; Conservative 79; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF-
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Best Local Similarity
Matches 130; Conserv
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                              Arithmes 155, 1955
Aritle: Complementary DNA characterization and chromosomal localization of a human gene ArReference number: JG4024, MUID:95237621; PMID:7721102
ArReference number: JG4024, MUID:95237621; PMID:7721102
Arrestates number: JG4024, MUID:95237621; PMID:7721102
Arrestates: LC0P
Arrestates: LC0P
Arrestates: LEMBL:X76400, NID:g732795; PIDN:CAA53980.1; PID:g732796
G.Genetics: Arrestates: EMBL:X76400, NID:g732795; PIDN:CAA53980.1; PID:g732796
Arross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
G.Genetics: Arrestates: GDB:583951
Arross-references: GDB:583951
Arross-references: GDB:583951
Arross-references: GDB:TOTO in mannoglobulin homology
G.Keywords: glycoprocein; transmembrane protein
F.1-30/Domain: signal sequence #status predicted crotein #status predicted Arrows
F.31-S18/Product: poliovirus receptor-related protein #status predicted
F.31-S18/Product: poliovirus receptor-related protein #status predicted
F.35-379/Domain: transmembrane #status predicted crotein
F.36-772,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted
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poliovirus receptor mPVR - mouse
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53437
C;Accession: A53437
C;Accession: A53437
J; Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with p A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Accession: A53437
A;Accession: A53437
A;Accession: A53437
A;Cross-references: MRVA
A;Residues: 1-530 cAOK>
A;Cross-references: UNPROT:932507; GB:D26107; NID:9475017; PIDN:BAA05103.1; PID:g825507
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           F.; Maroc,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
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       F.; Bardin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%; Score 54%;
33.4%; Pred. No. 2.6e-32;
tive 68; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 495.5; DB 2; Length 930.6%; Pred. No. 1e-28; ive 72; Mismatches 188; Indels
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A,Note: sequence extracted from NCBI backbone (NCBIN:146664,
C.Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>
   F.; Mattei, M.G.; Gabert, J.; Birg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 33.49
Matches 119; Conservative
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Best Local Simil
Matches 133; C
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243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302

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30 LLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT

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C,Accession: 153960
K; Eberle, F; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Accession: 153960
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: A second gene for the African green monkey poliovirus receptor that has no puta. A,Reference number: A44194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF-K 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44192
R;Kolke, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that
                                                                                                                 C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF------KNYSLNDATITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PPTP----LLWPLALLILLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFFKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: Q9UEI6; GB: S79171; NID: g1042202; PID: g1042203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.8%; Score 455; DB 2; Length 47
Best Local Similarity 30.3%; Pred. No. 8.3e-26;
Matches 121; Conservative 67; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                         ;Superfamily: poliovirus receptor; immunoglobulin homology
;276-331/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WGAVGGTLLVLLLAGGFLALILLRGRRRKS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Superfamily: poliovirus receptor; immunoglobu F, 259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48817
                                                                                                                                                                                                                                                                                                              A; Residues: 1-478 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: B44194
                                                                                                  PRR2 alpha - human
                                                                                                                                                                                                                                                                                                                                                                     A;Gene: PRR2alpha
C;Superfamily: pol
F;276-331/Domain:
    352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
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                                                                                                                                                                                                                                                                                                                                         VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
                                                                                  295 DWSTISGIFPISAVAQGSQL-VIHAVDSLFNITFVCTVINAVGMGRAEQVIFVRETP--N 351
                                                                                                                                                           |: | :| | :: | | | | TAGAGATGGILGGIGGILGATAVAATGILICRQQRKEQTLQGAEEDEDLEGPPSYKPPTP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QISWEKIHGKSSQTVAVHHPQYGFSVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 VEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAQEVTIGPQSV-----AVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTS---SIAV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 FSDSGKYICKAVTFPLGNAQSSTTVTVLVEP----TVSLIKGPDSLIDGGNETVAAICI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIISQYKLFPTRFARGRRITCVVKHP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 STGGRPPARITWISSLGG-EAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPPTHKPP-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 LLQPPTPPPLLLLLFPLLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKC--LIEVNETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VLPPSRLSPTLPLLPLLLLLQETGAQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.3%; Score 467; DB 1; 32.5%; Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AGAVIGAVLALFIIAIFVT-VLLTPRKKRPS 398
                                                                                                                                                                                                                                        : : : | | : |::
112 KAKLBAQEMPSQ-LFTLGASEHS 433
                                                                                                                                                                                                               415 LYEERSPPLPQKDLFQVCVHEYT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.3
Best Local Similarity 32.5
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312
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297

K.; Takeç

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A;Accession: A43024
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Coss-references: UNIPROT:PI5151; EMBL:X64116
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and example for number: A90910; MuID:89168426; PMID:2538245
A;Reference number: A90910; MuID:89168426; PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-6.7, A, 68-392 <MEN>
A;Cross-references: GB:M24406
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Cross-references: GDB:120124; OMIM:173850
A/Apa position: 19913.2-19943.2
A/Introns: 27/1; 143/1; 242/1; 281/2; 331/1
A/Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane prof/F; 20/Domain: signal sequence #status predicted <SIG>F; 1-30/Domain: sextracellular #status predicted <EXT>
F; 21-33/Product: poliovirus receptor delta #status predicted <MAT>
F; 21-33/Domain: immunoglobulin homology <IMM1>
F; 159-23/Domain: immunoglobulin homology <IMM3>
F; 344-367/Domain: immunoglobulin homology <IMM3>
F; 344-367/Domain: intracellular #status predicted <IMM>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
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F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status predicted <IMT>
F; 368-392/Domain: intracellular #status 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           produced both as membrane-bound and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A43024; B31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, A;Title: The poliovirus receptor protein is produced both as membrane-bound and A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 -HGESGSMAVFHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTPPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                           298 LIRPVDKPINTTFICHVTNALGARQAELTVQVKEGPPSEPSGMSSNIIIFLILGIVILLT 357
264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLH 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 FPLLLESRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG
                                                                                                                       324 FVHPLIFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALF
                                26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 392
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Best Local Similarity 29.3%; Pred. No. 5.1e-22;
Matches 106; Conservative 67; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poliovirus receptor splice form delta precursor - human
N/Alternate names: poliovirus receptor H20B
                                                                                                                                                                                                                                                      381 IIAIFV 386
                                                                                                                                                                                                                                                                                                                358 LLGİGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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poliovirus receptor (clone AGM-alpha-1) - green monkey
poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44194
R;Koike, S:; Ise, I.; Sato, Y:; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Reference number: A44194
A;Gtatus: preliminary
A;Gtatus: preliminary
A;Gtatus: preliminary
A;Gtatus: preliminary
A;Gtatus: preliminary
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology < IMM>
                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 WEGDLGEMESTITS--FPNETAIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL 263
                                                                                                                                                                                                                                                                                                                             CKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 DIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 FVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEKIHGKSSQTVAVHH---PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEGDLGEMESTTTS--FPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFIL 263
                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 PPLLITILEL---SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT
                                                                                                    Gaps
                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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                                   Length 392;
                                                                                                                                                              PPLLLLLFPLLLFSRLCGALAGPIIVE--PHVTAVWGKNVSLKCLIEV
                                ; Score 418; DB 2; Length 39; Pred. No. 3.4e-23; 64; Mismatches 162; Indels
                                      18.2%;
30.6%;
                                      Query Match
Best Local Similarity 30.64
Matches 112; Conservative
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LLGIGV 363
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R;Chadeneau, C.; LeMoullac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinom A;Reference number: A54017; MUID:94253144; PMID:8195207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q7M048; GB:L12025
R;Chadeneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcin.
A;Reference number: A61206; MUID:91184910; PMID:2010233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
MyResidues: 34-41, 7X',43-53 <CH2>
A;Note: the residue at position 9 is suggested to be glycosylated asparagine
C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cel
C;Keywords: glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                386
                                                                                       VTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                              242 YPPEVSISGYDNNWYLGQNEATLTCDARSNPEPTGYNWSTTMGPLPPPAVAQGAQL-LIR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AVWGKNVSLKCLI--EVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLF-K 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 GFLGGSTVLHCSLASKDNVTITQLTWMKRDPDGSPFRACLPPQEGPSISDPERVKFLVAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDGGNETVAAICIAATGKPVAHIDW----EGDLGEMESTTTSFPNETATIISQYKLFPTR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 MPQD----VAKCISADGHPPGRITWSSNVNGSYREWKETGSSRAPPQLSATSPWCLLARQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTPPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG
                                                                                                                                                                        DLGEMESTT--TSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQ
                                                                                                                                                                                                               DLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY
                                                                                                                                                                                                                                                                                                           267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH
                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGAVIGAVLALFIIAIFV
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A;Residues: 1-416 <CHA>
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A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
A;Gene: GDB:PVR; PV8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Alternate names: poliovirus receptor beta
S;Contains: poliovirus receptor beta
C;Species: Home sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
R;Kolke, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: $12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-417 < KOIS
A; Residues: 1-417 < KOIS
A; Cross-references: UNIPROT: PISISI; UNIPROT: Q96BJ1; EMBL: X64116; NID: g35809; PIDN: CAA454
A; Note: 67-Ala was also found
A; Note: 67-Ala was also found
A; Note: the gamma form has 331-Gly and lacks residues 332-384
A; Note: the gamma form has 331-Gly and lacks residues 332-384
A; Note: the gamma form has 331-Gly and lacks residues 332-384
A; Note: the gamma form has 331-Gly and lacks residues 332-384
A; Note: the gamma form has 331-Gly and lacks residues 332-384
A; Fitle: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A; Reference number: A90910; MUID: 89168426; PMID: 2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-66,7A', 68-417 <MEN>
A;Residues: references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
||| | :| : | : | : | : | : DLGGMPNTSQVPGFLSGTVTVTSLWILTVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
                                                                                                  YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
                                                                                                                                                PLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIAVAGAVIGAVLALFIIAIFV 386
                                                                                                                                                                                                                                                                       - HGESGSMAVFHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 IHGKSSQTVAVHH----PQYGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 FPLILLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                      387
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F;1677-3686/Domain: IV < DOM4>
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A;Residues: 2166-2171,'X'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A40306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: HSPG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                    irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)
Nylternate names: irrec-roughest protein
C,Species: Drosophila melanogaster
C;Date: 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49448; S34129
R;Ramos, R.G.F.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst
Gense Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proje
A;Reference number: A49448; MUID:94102535; PMID:7503814
A;Recession: A49448
A;Residues: 1-764 <RAM>
A;Residues: 1-764 <RAM>
A;Cross-references: UNIPROT:Q08180; GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NI
C;Gene: FlyBase:rst
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A38096

perlecan precursor - human
NyAlternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote
C;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
C;Accession: A38096; S19256; S77946; A41055; A40306; B33625; A33625; A41736
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Blol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL-----NDATITLHNIGFSDS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 VAHIDWEGDIG-----EMESTITSFPNETA-TIISQYKLFPTRFARGRRITCVVKHPALE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYI-CKVTNSLGQRS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECRADANPSDVRYRWFIND----EPIIGGQKTEMVIRNVTRKFHDAIVKCEVQNSVGKSE 335
PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSG-VYICKVTNSLGQRSDQKVIYIS 356
                                          279 PPINYSWSTATGPLPNSTHFQENGSHLLISTVDDLNNTIFVCKAINALGSGQGQVTILV- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 GKYICKAVTFPLGNAQSSTT---VTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDIRYSFI-LDIQYAPEVSVT-----GYDGNWFVGRKG-------VNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLFPLLLFSRLCGAL-AGP-----IIVEPH-VTAVWGKNVSLKCLIEVNETITQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 229.5; DB 2; Length 24.2%; Pred. No. 5.8e-09; ive 65; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : : | | | : | | : | DSETLDISYAPSFRORPOSMEAD--VGSVVSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOKVIYISDVP-FKQTSSIAVAGAVIGAVLAL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.2'
Matches 95; Conservative
                                                                                              357 DVPFKQTSSI 366
                                                                                                                                          ----KEASEI 343
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65;

5175;

Length Indels 174

891 234 943

847

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hemicentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11.-Jan-2000 #sequence revision 11.-Jan-2000 #text_change 09-Jul-2004
C;Accession: T41290; T2093; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: X
A;Introns 85/1, 120/1, 334/3; 370/1, 477/2, 606/3; 664/1, 935/3; 977/1; 1051/3; 1184/3;
A;Introns 85/1, 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Modidues: 1-5198 <WI2>
A; Residues: 1-5198 <WI2>
A; CESP: F15G9.4b
A; Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 PTRFARGR---RITCVVKHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                      117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT---VTVLVEPTVSL
                                                                                                                                                                                                                                                                                                                                                             -----NLLITDAQI-----BDQGQFTCIARN-TYGQQSQSTTLMVTGLVSPVLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                 175 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              892 VPPEEQLIEGQDLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FVGRKGVNLKCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVH
                                                                                                                                                                                                              793 PTIIESPHTVRVNIERQVTLQCL-AVGIPPPEIEWQK---GNVLLATLNNPRYTQLADG-
                                                                                                                                                  59 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGE
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26.4%; Pred. No. 1.8e-05;
ative 42; Mismatches 138; Indels 65;
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       Query Match
8.5%; Score 196.5; DB 2;
Best Local Similarity 26.4%; Pred. No. 1.8e-05;
Matches 88; Conservative 42; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTP 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 PLIFNYSGVYICKVTNSLGQRSDQKVIYISDVP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
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A;Reference number: Z19355
A;Accession: T20993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T43290
A;Status: preliminary; translated from
A;Molecule type: mRNA
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 848
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Cispecies: Caenorhabdiis elegans
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipatesion: T20932; T24733
Cipatesion: T20932; T24733
Cipatesion: T20992
A;Reference number: Z19355
A;Reference number: Z19355
A;Reference number: Z19355
A;Reference number: Z19355
A;Residues: 1-5175 < WILD
A;Residues: 1-5175 < WILD
A;Residues: 1-5175 < WILD
A;Residues: 1-5175 < WILD
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A;Residue
F;3888-3921/Domain: EGF homology <EGF>
F;3953-4106/Domain: laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
F;4149-4151/Region: mcfor neuron attachment (L-R-E) mctif
F;4290-4301/Region: mcfor neuron attachment (L-R-E) mctif
F;67,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F;895,721,775,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMEL:247070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics
A;Gene: CESP:F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2882/1; 2889/3; 2913/3; 2911/1; 2017/1; 1051/3; 1184/3; 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3074 SIIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLSVHGPPTVSVLPEGPVWVKVG 3127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPIIVE---PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 KGVNLKCNADANPPPFKSVWSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYIC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARTLRPSPLCPGGGKAQLS-SASLLGAGLL--LOPPTPPPLLLLLFPLLLFSRLCGALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 -LVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI-LDIQYAPEVSVTGYDGNWFVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEYOGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTV-----
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                           DB 2; Length 4391;
                                                                                                                                                                                                                                                                                                                       Query Match
8.9%; Score 205.5; DB 2; Length 4
Best Local Similarity 23.9%; Pred. No. 3.1e-06;
Matches 90; Conservative 60; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
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A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule typeliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-5175 <WIZ>
A;Residues: 1-5175 <WIZ>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 KVTNSLGQRSDQKVIYI 355
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Gaps

65;

Search completed: October 6, 2005, 10:21:12 Job time : 15.3671 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02; Search time 64.8231 Seconds

(without alignments)

3452.143 Million cell updates/sec
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3452.143 Million cell updates/.
Title: US-09-972-268-31
Perfect score: 2299
Sequence: 1 MARTLRPSPLCPGGGKAQLS.......ERSPPLPQKDLFQVCVHBYT 437

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	otion	mus musculu	mus musculu	homo sapien	homo sapien	_	mus musculu	homo	homo sapien	homo sapien	mus musculu	mus musculu	homo sapien	sus scrofa	mesocricetu	cercopithec	bos taurus	homo sapien	homo sapien	xenor	mus musculu	mus musculu	mus musculu	mus musculu	_	homo sapien	xenopus lae	mus musculu	mus musculu	homo sapien	cercopithec
	Description	Q9j1b8	Q9j1b7	O9ngs3	Q6nvz3	Q9 j 1b9	900060	Q8nc05	Q9y412	Q9bva9	Q9jkf6	6m6d90	015223	099176	Q9erf5	09g174	09g175	Q96ny8	Q96k15	Q6g125	P32507	080xj5	6dqp60	08ced8	Q8r007	092692	Q66j72	Q8c6£2	Q91vt9	Ognei6	P32506
SUMMARIES	ID	Q9JLB8	Q9JLB7	O9NQS3	Q6NVZ3	Q9JLB9	90006Ö	QBNC05	Q9Y412	Q9BVA9	PVR1 MOUSE	<u> 06Р9М</u> 9	PVR1 HUMAN	PVR1 PIG	Q9ERF5	Q9GL74	Q9GL75	Q96NY8	Q96K15	Q6GL25	PVR2 MOUSE	Q80X J 5	Q9DBP8	QSCEDS	Q8R007	PVR2 HUMAN	Q66J72	QBC6F2	Q91VT9	Q9UE16	PVR CERAE
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	f Query Match Length DB	510	438	549	366	549	549	267	407	304	515	515	517	515	295	298	295	510	510	464	530	530	483	508	508	538	463	467	467	449	417
	Query Match	91.7	91.6	82.8	81.4	78.4	76.5	53.7	50.4	27.4	25.2	25.0	24.6	24.6	23.2	23.0	22.9	22.7	22.7	21.6	21.6	21.6	21.5	21.5	21.5	21.3	21.2	20.3	20.3	18.6	18.2
	Score	2108	2107	1902.5	1872	1803	1759	1235	1159.5	630.5	580	575	566.5	564.5	534.5	528	526.5	522	521	497.5	495.5	495.5	494	494	494	490	488	467	467	427.5	418
	Result No.		~	ო	4	ß	y	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

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Q8hy1	06361	P1515	Q91wp	Q8K094	Q8bvf	Q0883	Q8hy1	Q8hy1	Q6097	Q7m04	Q7tnl	9yd60	066kx
Q8HY16	963611	PVR HUMAN	Q91WP1	Q8K094	Q8BVF6	008835	Q8HY15	Q8HY14	060977	Q7M048	Q7TNL1	Q9BY67	Q66KX2
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-			ß	5.	5.	395	390	386	55.5	6.5	309	5.5	4.5
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ALIGNMENTS

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                                                                                                                                                                       301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNSLGQRSDQXVIYISDIPL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGGRSDQKVIYISDPPT 360
                                                                                                                                                                                                                                                                 361 TQTSSIAVAGAVIALFIITVFVTVLLTPRKKRPSYLDKVIDLPPTHKPPVYEER1 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
181 LIDGGNETVAAVCVAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTRFAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Gene 0:0-0(2000).
                                                                        241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVLVEPTVSLIKGPDS
                                                                                                                                              KSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDOKVIYISDVPF
                                                                                                                                                                                                                                             361 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARTIRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelt
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF282874; AAF97597.1; -.
InterPro; IPR001559; IG.
InterPro; IPR00110; IG-like.
Pfam; PF00047; ig; 1.
SWART; SM0409; IG; II.
SRART; SS0035; IG LIKE; 3.
SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.8%; Score 1902.5; DB 2, 79.3%; Pred. No. 2.6e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 79.3%; Pred. No. 2.6e-
Matches 372; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 AA
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01-027-2000 (TrEMBLrel. 15,
01-0CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       421 PSLPOKDL 428
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                                                                                                                                              301
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                                                                                                                                                                       KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420
  181 LIDGGNETVAAVCVAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTRFAR 240
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MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
Satch-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
Tachibana K., Mizoguchi A., Takahashi K., Miyahara M.,
"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion
                                               61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHDQYGFSVQGDYQGR
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                                                                                                                                              KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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91.6%; Score 2107; DB 2; Length 438;
Best Local Similarity 93.2%; Pred. No. 2.4e-155;
Matches 399; Conservative 12; Mismatches 17; Indels
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InterPro; IPR007110; Ig-like.
Pfam; PP00047; ig; 1.
SMART; SM0409; IG; 1.
PROSITE; PSS0335; IG LIKE; 3.
SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;
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Last annotation update)
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EMBL; AF195835; AAF63687.1; -.

MGD; MGI:1930171; Prv13--.

GO; GO:0005913; C:cell-cell adherens junction; IDA.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0005615; F:protesin binding; IPA.

GO; GO:0005515; F:protesin binding; IPA.

GO; GO:0016337; P:cell-cell adhesion; IDA.
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                                                                                                                                                                                                                                                                                                                                          PPLPQKDLFQVCVH 434
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                                                                                                                                                    61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR
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                                                                                                          LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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BEMBL, AF195833, AAF63685.1; -

MGD; MGI:1930171; Pvr13.

GO; GO:0005913; C:cell-cell adherens junction; GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016515; F:protein binding; IPI.

GO; GO:0016317; P:cell-cell adhesion; IDA.
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InterPro, IPR007110; Ig-like.
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Matches 357; Conservative
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SMART; SM00409; IG;
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SEQUENCE FROM N.A.
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophywis S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia, G. W., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Anting M., Madan A., Young A.C., Schmutz J., Myers R.M., Butterfield Y.S.,
Anting M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Annes S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
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InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
SMART; SM00409; Ig; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64;
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STRAIR=C57BL/G47 IISSUE=Whole body;
MEDLINE=C57BL/G47 PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=C37BL/G499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                        enriched library, clone:2610301B19 product:poliovirus receptor-related
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                                                     KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                                                                                                                             ----PSYLDKVIDLPPTHK-----PPPLYEERSPP---
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-langth cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUB=Whole body;
MEDLINB=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
BIBLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MIKEN FANTOM CONSORTIUM;
"FUNCTIONAL annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 17,
                                                                                                                                             IFVTVLLTPRKKR----
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   full insert sequence.
                                                                                                                                                                                                                          488
                                                                                                                                                                                                LPQKDLFQ 430
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                         LIRKDYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                     01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                  Name=Pvrl3
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

RAGACH J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

Addachi J., Alzawa K., Akahira S., Pukudi Shi, Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Arakawa T., Bani Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Innorani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Saaki D., Shibata K., Shibata Y., Sakal C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Sakal C., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Rajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

R. India Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

R. Lamitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R. Shill, Akoll1999171; Pvr13.

R. GO; GO:0005913; C:cell-cell adherens junction; IDA.

R. GO; GO:0016515; F:protein binding; IPI.

R. GO; GO:0016515; F:protein binding; IPI.

R. Correspondent Dinding; IPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | : | : | | : | | ILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYPDSVKKENKNPVNN 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFVTVLLTPRKKR------PSYLDKVIDLPPTHK-----PPPLYEERSPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IVEPHYTAVMGKNVSLKCLIEVNETITQISWEKIHGKKSTQTVAVHHPQYGFSVQGDYQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 TITLOPTVQWHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGGALFLVLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Iudivake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.5%; Score 1759; DB 2; 71.5%; Pred, No. 3.7e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Mismatches
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J., Wiemann S.;

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241 EPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFCYRRRTFRGDYFAK- 299
                                                                                                                                                                                                                                                                                                                                                                                             246 CVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                               LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDKV 403
                                                                                                                                                                                                                                                                                                                                   1 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA 60
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                                                                                                                                                                                                                                                                                                   SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA
                                                                                                                                                                                                                                                                                                                                                                            203 HIDWEGDLGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                               DB 2; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 304;
                               Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; ALOSOO71; CA443256.1; -. PIR; T08732; T08732. DIR. InterPro; IPR007110; Ig-like. PROSITE; PS50835; IG_LIKE; 2. Hypothetical protein. In 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Indels
                                                                                                                                                                                                                                                                32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, BC001336; AAH01336.1;
INTERPTO; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Similar to nectin 3; DKFZP566B0846 protein (Fragment).
                                                                                                                                                                                             407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 630.5; DB 2; 56.7%; Pred. No. 9.9e-41;
                                                                                                                                                                                                                             Query Match 50.4%; Score 1159.5; DB 2 Best Local Similarity 70.3%; Pred. No. 1.1e-81; Matches 230; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 IDLPPTHKPPPLYEERSPPLPQKDLFQ 430
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                  FROM N.A.
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[1]
SEQUENCE 1
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SEQUENCE
                                                                                                                                                                                                                                                                                                       143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPPNETATIISOYKLEPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LIRGPLIPRSFSGNPRALAGPIIVEPHVTAVWGRNVSLKCLIEVNETITQISWEKIHGKS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 LLLFPLL--LFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKS
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSY412:
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKPZp566B0846 (Fragment).
Name=DKFZp566B0846;
Name=DKFZp566B0846;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 53.7%; Score 1235; DB 2; Length 267; Local Similarity 96.0%; Pred. No. 8.2e-88; nes 242; Conservative 0; Mismatches 8; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;
                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                          267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                              Hypothetical protein FLJ90624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro, IPR003599, Ig.
Interpro, IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; ISSMART; SM00409; IG; 1.
 LPQKDLFQ 430
                                   LIRKDYLE 488
                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
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                        61 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTLQ 120
                                                                                                                     | : :|:| | :::: : 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 
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MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
MEDLINE=20243787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
Leccoq B., Dubreuil P., Campadealli-Fiuwe G.;
"The murine homolog of human nectini delta serves as a species
nonspecific mediator for entry of human and animal alpha herpesviruses
in a pathway independent of detectable binding to gD.";
proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                         ----FKQTSSIAVAGAVIGAVLALFIIAIFVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry into
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                                                                                                                                                                                                                                                                                                                                                   PWRI MUSE STANDARD; PRT; 515 AA.

09JKF6; Q9ERL5; Q9J117;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).

Name=Pvrl1; Synonyms=HveC, Prrl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20541977; PubMed=11090177;
DOI=10.1128/JVI.74.24.11773-11781.2000;
Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
"Striking similarity of muxine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Interacts with HSV glycoprotein D (gD).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhan J., Wimmer E.; "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed floor plate during embryogenesis, suggesting a role in neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Probably involved in cell adhesion. Receptor alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus)
                                                                                                                                                                                        LLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430
                                                                                                                                                                                                                                        181 FCYRRRRFRGDYFAK-----NYIPPSDMQKES----QIDVLQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alphaherpesvirus entry.";
J. Virol. 74:1173-11781(2000).
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STRAIN=Swiss Webster;
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104 FIDGTIRLSGLELEDEGMYICEFATFPTGNRESQLNLTVWAKPT-NWIEGTRAVLRARKG 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 SLACIVNY-HLDR-FRESLTLAVQYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY
                                                                      Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Gaps
                                                                                                                                                                    protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 515;
                                                                                                                                                                  Poliovirus receptor related
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Mismatches 130; Indels
                                                                                                                                                                                                  Potential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
Poly-dlu.
Poly-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFF608EBSFFB7A0F CRC64;
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Last annotation update)
GO; GO:0005913; C:cell-cell adherens junction; IDA.GO; GO:0005915; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; IDA.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L -> P (in Ref. 1).
N -> D (in Ref. 1).
P -> PP (in Ref. 2).
S -> G (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                By similarity.
By similarity.
By similarity.
N-linked (GlCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 580; DB 1;
Pred. No. 1.7e-36;
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                                                                                                                                                  Potential.
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N-linked
N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57064 MW;
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36.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                 Signal; Transmembrane SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
428
428
515 AA;
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STAINS-C57BL/6; TISSUB-Brain;

MEDLINE-238255; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brapleron M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

A Rapleron M., Soares M.B., Robaldy S.J.,

A Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Broak S.A., McKwan P.J., McKernan R.J., Malk J.A., Gunarane P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Dones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTDVVLHCSFANPLPSVKITQVTWQKASNGSKQNMAIYNPTMGVSVLPPYEKRVEFLRPS 103
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; Score 575; DB 2; Length 515; 36.4%; Pred. No. 4.1e-36; ive 68; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC06.694; AAH66.94.1; -. CO, GO:0005913; C:cell-cell adherens junction; IDA. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0006815; F:procein binding; IPI. GO; GO:0008872; F:proceptor activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00406; IGc2; 2.
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281 HWTTLNGSLPKGVEAQNRTLFFRGPITYSLAGTYICEATNPIGTRSGQVEVNITEPPYTP 340
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-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA characterization and chromosomal localization of a gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 28-517 FROM N.A.. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE=20392396; PubMed=10932188; DOI=10.1038/78119; SUZUKI K., Hu D., BUBTOS T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.; "Mutations of PYRL1, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spear P.G.; "Entry of alphaherpesviruses mediated by poliovirus receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-99279152; PubMed-9616127; DOI=10.1126/science.280.5369.1618;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE-95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DODE-10.1128/JVT.7.75.12.5684-5691.2001;
LODEZ M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
Campadelli-Fjume G., Dubreuil P.;
Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectini (or prri-Hige-Hvec) modulates positively and negatively susceptibility to hsv infection.";
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د
                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q15223-3; Sequence=VSP 002624, VSP 002625; DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1
                                                                                                                                                                          PVR1 HUMAN STANDARD; PRT; 517 AA.

Q15223; O75465; Q9HBE6; Q9HBW2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last sequence update)
05-UJU-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (1)
                                       363 TSS-----IAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Genet. 25:427-430(2000).
-!- FUNCTION: Probably involved in cell adhesion. Receptor
alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus)
                                                              IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Delta;
IsoId=Q15223-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 1 and poliovirus receptor."; Science 280:1618-1620(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM GAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the poliovirus receptor gene."; Gene 155:261-265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21256041; PubMed=11356977
                                                                                                                                                                                                                                                                                                                                          Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virol. 75:5684-5691(2001).
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          (CD111 antigen).
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Q9GL76;
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                                                                                                                                                                SEQUENCE
VARSPLIC
                                                                                                                                 VARSPLIC
                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
responsible for allelic forms known as Margarita island ectodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> AFCQLIYPGKGRTRARMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poliovirus receptor related protein 1. Extracellular (Potential). Potential.
             dysplasia [MIM:225060] and Zlotogora-Ogur syndrome. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. DATABARSE: NAME-EROW; NOTE-EROW 2:45-49(2001); WWW-nhttp://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
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Missing (In isoform Gamma).
/FTId=VSP 002625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART, SM0406; ÍGv. 1.
PROSITE; PS50835; IG LIKE; 2.
Alternative splicing; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform Gamma).
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Ig-like C2-type 1.
Ig-like C2-type 2.
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By similarity.
By similarity.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFPYTPSPPEHGRRAGPV
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InterPro; IPRO07110; Ig-like.
Ffam; PF00047; ig; 2.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GlcNAc.
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Poly-Gly.
By similarity.
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AAG16648.1; JOINED.
AAG16649.1; JOINED.
AAG16649.1; OINED.
AAG16649.1; JOINED.
AAG16649.1; JOINED.
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AAG16649.1; JOINED.
AAG16649.1; JOINED.
AAG16649.1; JOINED.
AAG16649.1; JOINED.
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                                                                                                                                                                                                                                                                                                                 AF196768; AAG16648.1; JOINED
AF196769; AAG16648.1; JOINED
AF196770; AAG16648.1; JOINED
                                                                                                                                                                                                                                                                 AF060231; AAC23798.1; -. AY029539; AAK33124.1; -. AF252867; AAG16648.1; -.
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EMBL; AF196773; AAG16649.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                        ALRRRRHTFKGDYSTKKHVYGNGYSKAGIPQHHPPMAQNLQ
YPDDSDDEKKAGPLGGSSYBEBEBEBEGGGGGERKVGGPHP
-> KPRPQRGLGSAARLLAGTVAVLILLVAVLTYFLYNRQ
GKSPPETDGAGTDOPLSGKEBEPSRQSSLVPEDIQVVHLD
PGRQQQEEBDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
ECP (in isoform Alpha).
/FIId=VSP_002626.
Missing (in isoform Alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 GKNVSLKCLIE---VNETITQISWEXIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 ODDKVLVATCTSANGKPPSVVSWETRLKGBAEYOEIRNPNGTVTVISRYRLVPSREAHOO 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
FPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 SLACIVNYHM--DRFKESLTLNVQYEPEVTIEGFDGNWYLQRMDVKLTCKADANPPATEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTRFARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is a functional alphaherpesvirus receptor.";
Virology 2811-315-388 (2001).
-!- FUNCTION: Probably involved in cell adhesion. Receptor for
alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine HveC, a member of the highly conserved HveC/nectin 1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
Name=PVRL1; Synonyms=HVEC, PRR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity)
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | : | | | :: | : | 341 SPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVAL--RRRRHTF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 TS------SIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                            DF34C8AEC893EE6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             24.6%; Score 566.5; DB 1;
35.2%; Pred. No. 1.9e-35;
ive 68; Mismatches 134;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCGALAGPIIVEPHVTAVWGKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 MGVSVIAPYRERVEFLRPSFTDGTIRLSRLELEDEGVYICEFATFPAGNRESQLNLIVWA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMDVKLTCKADANPPATEYHWTTLNGSLPKGVBAQNRTLFFRGPINYSMAGTYICEATNP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPTVSLIKGPDSLIDG----GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 KPT-NWIEGTQAVLRAKKGKDDKVLVATĆTSANGKPPSVVSWETHLKGEAEYQEIRNPNG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGQRSDQKVIYISDVPFKQTS-----SIAVAGAVIGAV-LALFIIAIFVTVLLTP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| || | : |:: |: | : 332 IGTRSGQVEVNITEFPYTPSPPEHGRRAGQVPTAIIGGVVGSILLVLFVVGGIVVALCRR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPGAHTQVVQVNDSMYGFIGTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPA 84
                                                                                                                                                                                                       Pfam; PF00047; ig; 2. 2-8Mart; sM00406; ig; 2. 1. PF0SITE; PS00406; ig; 1. PF0SITE; PS50835; ig LIEE; 2. Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                             Poliovirus receptor related protein 1.
Extracellular (Potential).
Potential.
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(Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 564.5; DB 1; Length 5 34.1%; Pred. No. 2.7e-35; ive 64; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linked (GlcNAc. . .) (Pc
BFAB00320DDE3785 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       | 19-1ike v-type. | 19-1ike v-type. | 19-1ike C2-type 1. | 19-1ike C2-type 2. | Poly-Glu. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. | Poly-Gly. 
                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential)
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                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                              EMBL; AF308632; AAG30281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57047 MW;
                                                                                                                                            HSSP, Q05793, 1GL4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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134; Conservative
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202
286
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SIGNAL 1 30
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515 AA;
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RESULT 14 Q9ERF5

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Mammalia, Eutheria, Primates, Cararrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
NCBI_TaxID=9534;
                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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SEQUENCE FROM N.A.
MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
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MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.2%; Score 534.5; DB 2; Length 295; Best Local Similarity 38.3%; Pred. No. 2.8e-33; Matches 113; Conservative 58; Mismatches 113; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33112 MW; 03E5C4DCB5032E7F CRC64;
                                                                    Last sequence update)
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                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequen
01-0CT-2003 (TrEMBLrel. 25, Last annota
Herpesvirus entry mediator C (Fragment)
                                                                                                                                                             Mesocricetus auratus (Golden hamster)
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
PRT;
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    PRELIMINARY;
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SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                                                                                                                                                              Cohen G.H.;
                                                                                                                                         Name=HveC;
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A Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
Cohen G.H.;

Toccine HveC, a member of the highly conserved HveC/nectin 1 family,
is a functional alphaherpesvirus receptor.";
Virology 281:315-328(2001).

R MBL, AR308635, AR3030284.1; -.
R InterPro: IPR003599; IG.
R InterPro: IPR001710; Ig-like.
R Fan; PR00407; Ig; 2.
R PROSITE; PS50835; IG LIKE; 2.
R PROSITE; PS50835; IG LIKE; 2.
T NON TER 298 AA; 33309 MW; AEAD41842B8CA200 CRC64;
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Best Local Similarity 37.6%; Pred. No. 9e-33;
Matches 112; Conservative 57; Mismatches 115; Indels 14; Gaps
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Search completed: October 6, 2005, 10:19:41 Job time : 65.8231 secs

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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Original Source: Hela Cell Line
OTHER INFORMATION: General Functional Class of Gene: Immunogl
OTHER INFORMATION: Superfamily
OTHER INFORMATION: Subcrimental Macromolecules: HSV-gD
OTHER INFORMATION: Subcellular localisation: Plasma Membrane
OTHER INFORMATION: Other Information: Viral Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.1%; Score 578; DB 4; Length 458; ilarity 35.5%; Pred. No. 2.1e-47; Conservative 65; Mismatches 157; Indels
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5.1.6
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US-09-949-016-11380
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US-09-949-016-7563
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US-09-944-10-20
US-09-778-510-20
US-09-778-510-4
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Gaps

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Original Source: Hela Cell Line General Functional Class of Gene: Immunoglobulin

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APPLICANT: Universita degli Studi di Bologna
APPLICANT: Universita degli Studi di Bologna
APPLICANT: Universita National de la Sante et de la Recherche M
APPLICANT: Institut National de la Sante et de la Recherche M
TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
TITLE OF INVENTION: BHV Infections
FILE REPERENCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
CURRENT APPLICATION NUMBER: US/09/435,956A
NUMBER OF SEQ ID NOS: 2
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SEQ ID NO 1
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US-09-915-524-19
US-09-915-524-19
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163 QDDKVLVATCTSANGKPPSVVSWETRLKGBAEYQEIRNPNGTVTVISRYRLVPSREAHQQ 222
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                  APPLICANT: MARTHEZ, Wanda M.
APPLICANT: MARTHEZ, Wanda M.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: COHEN, Gary H.
APPLICANT: COHEN, Gary H.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: WHITBECK, Claude
APPLICANT: WHITBECK, Claude
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFREENCE: 200290.0050/2UJ
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR APPLICATION NUMBER: PCT/US99/12235
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
LENGTH: 517
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Patent No. 6673545;
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS;
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172;
CURRENT APPLICATION NUMBER: 05/22,469
PRIOR APPLICATION NUMBER: 60/22,469
PRIOR PRIOR APPLICATION NUMBER: 60/22,469
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Best Local Similarity 35.2<sup>3</sup>
Matches 122; Conservative
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; Bequence 11380, Application US/09949016
; Betent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOOD1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/211,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11380
; LENTH: SI4
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                                                                      363 TSSIAVAGAVIGAVLALFIIAIFVTV--LLTPRKKRPSYLDKV-IDLPPTHKPPPLYEER 419
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                                                                                                                                         341 RGLGSAARLLAGTVAVFLILVAVLTVFFLYNRQQKSPPETDGAGTDQPLSQKPEPSPSRQ 400
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Patent No. 6641818
GENERAL INFORMATION:
APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARNER, Morgyn S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 122; Conservative
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US-09-949-016-11380
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ORGANISM: Human
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                                                                 211 GEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPE 270
                                                                                                                                                                                                                                                                                         VSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTF 330
                                                                                                                                                                                                                                                                                                                                                306 VSISGYDDNWYLGRIDATLSCDVRSNPEPTGYDWSTTSGTFPTSAVAQGSQL-VIHAVDS 364
                                                                                                                                                                                                                                                                                                                                                                                                                           331 NYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSSIA--VAGAVIGAVLALFIIA--IFV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ::| |||::| ::||:: :||:: :||:: :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|::|:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 VAAICIAATGKPVAHI-----DWEGDLGEMESTTTSFPNETATIISOYKLFPTRFARGR 242
                              ---- DWEGDL 210
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TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REPERENCE: 200290.0050/2U1
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR PILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-02
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19.9%; Score 458.5; DB 4;
Best Local Similarity 30.2%; Pred. No. 9.6e-36;
Matches 121; Conservative 66; Mismatches 160;
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WARNER, Morgyn S.
GERAGHTY, Robert G.
MARTINEZ, Wanda M.
MONTGOMERY, Rebecca I.
COHEN Gary H.
EISENBERG, Roselyn J.
WHITBECK, Charles J.
KRUMMENACHER, Claude
UNIVERSITY OF PENNSYLVANIA
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425 FILLRVRRRKS 436
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SOFTWARE: Patentin Ver. 2.1
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; Sequence 7563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VEWTER, U. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REFERENCE: CL001307
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTHARE: PSELSEQ for Windows Version 4.0
    SEQ ID NO 7563
    LENTH: 522
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                                                                                                                                                                                                                                                                                                      104 FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQLNLTVWAKPT-NWIEGTQAVLRAKKG 162
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                                                                                                                                                                                                                                                                                                                                                                                                128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 -GNETVAAICIAATGKPVAHIDWE------GDLGEMESTTTSFPNETATIISQYKL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 FPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 RPSPLCP-GGGKAQL-SSASLLGAGLLL---QPPTPPPLLLLLFPLLLFSRL-CGALAGP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 YISDVPFKQTS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSY 399
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                                                                                                                           Query Match 23.7%; Score 544; DB 4; Length 516 Best Local Similarity 33.4%; Pred. No. 5.3e-44; Matches 119; Conservative 68; Mismatches 129; Indels
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20
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Best Local &
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ORGANISM: Human
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US-09-949-016-7564
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Squence 6278, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTYON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTYON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTYON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 ISWEKIHGKSS-QTVAVHHPQYGFSVQGEYQG--RVLF------KNYSLNDATITL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSLIDGGNET 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 VAAICIAATGKPVAHI-----DWEGDLGEMESTITSFPNETATIISQYKLFPTRFARGR 242
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                                                                                                              303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 362
                                                                                                                                        13 PPTP-----LUMPLLLLLLLLTGAQDVRVQVLPBVRGQLGGTVELPCHLLPPVPGLYISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.9%; Score 458.5; DB 4; Length 479; 30.2%; Pred. No. 9.6e-36; Live 66; Mismatches 160; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
                                                                                                                                                                                                                             : | | | | | | :: | :: | | :: | | 354 PRDVGPLVWGAVGTLLVLLLAGGSLAFILLRVRRRRKS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.9
Best Local Similarity 30.2
Matches 121; Conservative
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RESULT 8

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Sequence 7564, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEASESEQ for Windows Version 4.0
SEQ ID NO 7564
LENGTH: 456
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 VKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRL 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQLLGATGMARAMAAAWPLLLVALLVLSWP---PPGTGDVVVQAPTQVPGFLGDSVTLPC
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Best Local Similarity 29.4
Matches 112; Conservative
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                                                                                            GNETVAAICIAATGKPVAHIDW----EGDLGEMESTITSPPNETAIIISQYKLFPTRFAR 240
                                                                                                                                                                     276 DMAGYNWSTNTGDFPNSVRRQGNMLLISTVEDGLNNTVIVCEVTNALGSGQGQVHIIVKE 335
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                                                                                                                                                                                                                               241 GRRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTGYDGNWFVGRKGVNLKCNADANPPP 299
                                                                                                                                                                                                                                                                                                               300 FKS--VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
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                                                                NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLI--DG 184
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FION: Molecules Designated B7L1
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-03
PRIOR APPLICATION NUMBER: US/09/778,17906
PRIOR APPLICATION NUMBER: 06/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
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US-09-778-510-20
: Sequence 20, Application US/09778510
; Patent No. 6512095
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US-09-778-510-20
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APPLICANT:
Baum,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          VTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 YAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 VTFPQGSRSVDIWLRVLAKPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 KNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSL 128
                                                                                                                                                                                                                                                                        44 FPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEK 93
                                                                                                                                                                                                                                                                                                9 WPLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTMTR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AQLARAT-----RSPLSWLLLLF-----CYALRKAGGDIRVLVPYNSTGVLG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGAL--AG---PIIVEPHVTAVWG
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Watson, James D
APPLICANT: Warison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 408;
                                                                                                                                                                                      Length 417;
                                                                                                                                                                                      17.5%; Score 402; DB 4; Length 41'
29.3%; Pred. No. 2.4e-30;
.ive 67; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 400.5; DB 3; Length 30.8%; Pred. No. 3.3e-30; Live 64; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR PELICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEO ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 4.0
    PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
                                                                                                                                                                                                                             106; Conservative
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123; Conservative
                                                                                                                                                                                                            Similarity
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                                                                                                       TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mouse
US-09-724-864-62
                                                                                                                              ; ORGANISM: Humar
US-09-949-016-6729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-724-864-62
                                                                                      LENGTH: 417
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Best Local S:
Matches 106
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PHVTAVWGKNVSLKCLIEVNETITQISWEKIHCKSSOTVAVHHPQYGFSVQGEYQGRVLF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 DGGNETVAAICIAATGKPVAHIDW-EGDL----GEMESTTTSFPNETATIISQYKLFPT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 RFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNAD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 ANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIY 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------KQTSSIAVAGAVLGAVLALFIIAIF 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2540PHZ ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
PILOR APPLICATION GATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 SPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALA----GPIIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SVVLPSGSQCAAAAAA------AAPPGLRLL---LLLFS--AAALIPTGDGQNLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 EG--EEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMY-----TVTSQLMLKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 304.5; DB 4; Length 25.2%; Pred. No. 8e-21; cive 76; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61, Application US/09944457; Patent No. 6734288; GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baten, Dan
APPLICANT: Baton, Dan
                                                                                                Godowski, Paul
Grimaldi, Christopher
                  Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 ISDVPF-----
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Best Local Similarity 25.2%
Matches 108; Conservative
                                                                                                                                        Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                               Kljavin, Ivar
                                                                                                                                                                                                 Napier, Mary
Roy, Margaret
                                                                                                                                                                                                                                                           Wood, William
                                                                                                                                                                                                                                         Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo Sapien
US-09-866-028-61
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APPLICANT:
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Sequence 1. Application US/09930803
Patent No. 6596493
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE SCHINGH, Muramaki
APPLICANT: YOSHINGH, Muramaki
TILE REFERENCE: JOHNSTOR AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JOHNSTOR APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEG-- 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELICEAIGKPQ 274
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                      PTIIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLI 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYS 127
---KQTSSIAVAGAVIGAVLALFIIAIFVTVL 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 306.5; DB 4; Length 442; 25.0%; Pred. No. 5.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Mismatches 173; Indels
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US-09-866-028-61
; Sequence 61, Application US/09866028
; Partent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.0 Matches 106; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                 394 ILGR 397
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PF----
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FILING DATE: No. 6734288ember 30,
APPLICATION NUMBER: PCT/US99/28301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 108; Conserv
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US-09-778-510-22
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APPLICATION UNBER: PCT/US99/28409
FILING DATE: NO. 6734286mbbr 30, 1999
APPLICATION NUMBER: PCT/US99/28313
                                                                                                                   Grimaldi, Christopher
                                               Gerritsen, Mary
Goddard, Audrey
                                                                                                                                            Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                                    Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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124 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLI 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 EG--EEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMY----TVTSQLMLKVH 208
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llarity 25.2%; Pred. No. 8e-21;
Conservative 76; Mismatches 167;
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Patent No. 6512095
GENERAL INFORMATION:
APPLICANT:
Baum, Peter
TITLE OF INVENTION:
FILE REFERENCE:
2844-US
1999
                                           PRIOR AFPLICATION NUMBER: FC1/US99/2001
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDTUARY 11, 2000
PRIOR PILING DATE: PEDTUARY 11, 2000
PRIOR PILING DATE: PEDTUARY 22, 2000
PRIOR PILING DATE: PEDTUARY 22, 2000
PRIOR FILING DATE: PEDTUARY 23, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR PILING DATE: PEDTUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
LENGTH: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 --LGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIQY 267
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                                                                                                                                                                                                                                                                                                                                                      3 PPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISC--QVNKSDDSVI--QL 58
                                                                                                                                                                                                                                                                                                                                  36 PPPL-LLLLFPLLLFSRLCGALAGPIIVEPHVTAVWCKNVSLKCLIEVNETITQISWEKI 94
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 60/095,663
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 22
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                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
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Search completed: October 6, 2005, 09:44:25 Job time : 19.301 secs

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Compugen Ltd.
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US-09-972-268-12
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries

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APPLICANT: Fanslow, William C.
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Jefton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PELING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 437
                                              Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 20, Appl
Sequence 20, Appli
Sequence 20, Appli
Sequence 31, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 114, Appli
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Sequence 1114, Appli
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Sequence 37, Appl
Sequence 34, Appl
Sequence 64, Appl
Sequence 66, Appl
Sequence 76, Appl
Sequence 54, Appl
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7, Appli
9, Appli
11, Appl
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Sequence 54, Al
Sequence 179,
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Sequence 7
Sequence 9
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4 US-10-161-572-45
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0 US-09-972-268-17
0 US-09-972-571-13
0 US-10-422-571-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
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ORGANISM: homo sapiens
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og qa		qq	361 KQTSSIAVAGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPLYEERS 420
y da	241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300	රු සි	421 PPLPQKDLFQ 430 421 PPLPQKDLFQ 430
% Q	301 KSUWSRLDGQWPDGLLASDNTLHFUHPLTFNYSGVYICKVTNSLGQRSDQKVIXISDVPF 360 	RESULT US-09-	RESULT 3 US-09-972-268-10
cy Gp	361 KQTSSIAVAGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420 	PUL GBI	Sequence 10, Application US/039/2288 Publication No. US20030044893A1 GENERAL INFORMATION: ApplicATT: Baum, Peter X.
S S	421 PPLPQKDLFQVCVHEYT 437 	4888E	FLICANT: FATILOW, WILLIAM C. PLICANT: LOTEON, Timochy E. PLICANT: Sorensen, Exic A. PLICANT: YOUAKIM, Adel THE OF INVENTION: NECTIN POLYPEPTIDES. POLYNUCLEOTIDES, METHODS OF MAKING AND USE THE
RESULT (US-09-9); Sequent (Public Reneral APPL); APPL	US-09-972-268-12 US-09-972-268-12 Sequence 12, Application US/09972268 Publication No. US20030044893A1 CENERAL INFORMATION: APPLICANT: Baum, Peter R. APPLICANT: Fanslow, William C.	CUR CUR CUR PRJ PRJ PRJ PRJ SOE	FILE REFERENCE: 3101-A CURRENT APPLICATION NUMBER: US/09/972,268 CURRENT FILING DATE: 2001-10-05 FRIOR APPLICATION NUMBER: 60/238,557 FRIOR APPLICATION NUMBER: 60/238,557 FRIOR FILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39 SEQ ID NO 10
APPL APPL APPL TITL FILE CURR	APPLICANT: LOICON, TAMOENY E. APPLICANT: Sorenia, Eric A. APPLICANT: Sorenia, Edic A. APPLICANT: Youakim, Adel TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T FILE REFERENCE: 3101-A CURRENT FILING DATE: 2001-10-05	0-SD	TENGENT 310 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are OTHER INFORMATION: from human Nectin-3 beta
•	PRIOR APPLICATION NUMBER: 6/238,557 PRIOR FILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin version 3.1	Mag Be	Ouery Match Best Local Similarity 99.5%; Score 2243; DB 10; Length 510; Best Local Similarity 99.5%; Pred. No. 2.88-164; Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
iii	EQ ID NO 12 LENGTHS 510 TYPE: PRT ORGANISM: homo sapiens	& 8	1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPLLLLLFPLLLFSRLCGALAGPI 60
US-09-97 Query Best I Matche	-09-972-268-12 Query Match Best Local Similarity 100.0%; Pred. No. 2.39-165; Marches 430: Conservative 0: Mismatches 0: Indels 0: Gaps 0:	δ DP	
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\ \delta \q		\dot \d	181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR 240
λο qa	VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGFDS	S G G	GRR.T.CVVKHPALEKDIRYGFILDIQYAPEYGYUGYDGNWFYGRKGYNLKCNADANPPPF
λ O	181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFFTRFAR 240 	δ a δ	KSVWSKLDGQWPDGLLASDNILHFVHFUTFNYSGVYICKVTNSLGQKSDQKVITTSDVFF 50 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIY1SDVPF 36
à	241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300	ර් යි	361 KQTSSIAVGANIGAVIALETIAIFVIYULITPRKKKRPSYLDKVIDLPFTHKPPPLKENS 420

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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR PELICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%; Score 2108; DB 10;
92.2%; Pred. No. 7.1e-154;
tive 12; Mismatches 22;
                                     APPLICANT: Kenichi TAXAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REPERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: CFT/JP01/01871
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09972268 Publication No. US20030044893A1 GENERAL INFORMATION:
Hiroyuki NAKANISHI
Keiko SATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 PPLPOKDLFQVCVH 434
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Matches 400; Conservative
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Sequence 8, Application US/09972268;
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE 1;
FILE REPREMENTE: 3001-10-05
CURRENT FILING DATE: 2001-10-05
PRIOR PAPLICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 3.3e-163;
tive 0; Mismatches 0;
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Publication No. US20030008334A1
GENERAL INFORMATION:
APPLICANT: YOSHIMI TAKAI
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                                              PPLPQKDLFQ 430
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ORGANISM: homo sapiens
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Best Local Similarity
Matches 424; Conservat
                       PPLPQKDLFQ
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US-09-959-845-4
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Sequence 19, Application US/09972268

Sequence 19, Application US/09972268

Publication No. US20030044893A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Fanslow, William C.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

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APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

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Best Local Similarity 93.2%
Matches 399; Conservative
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APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT APPLICATION NUMBER: PCT/JP01/01871
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: JP 2000-065595
NUMBER OF SEQ ID NOS: 14
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SOFTWARE: PatentIn version 3.1
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| PSLPQKDLLGQTEH 434
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Best Local Similarity 92.29
Matches 400; Conservative
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SEQ ID NO 6
LENGTH: 438
TYPE: PRT
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Best Local Similarity 93.23
Matches 399; Conservative
                                              LENGTH: 510
TYPE: PRT
ORGANISM: mus musculus
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US-09-959-845-6
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                   SEQ ID NO 18
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APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
APPLICANT: Timothy E.
APPLICANT: Timothy E.
APPLICANT: Jorden, William C.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYBEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: S95
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Best Local Similarity 99.5%; Pred. No. 1.1e-138;
Matches 363; Conservative 0; Mismatches 2;
                                                                                                                                                                  ; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
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APPLICANT: Baum, Perer R.
APPLICANT: Fanslow, William C.
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ORGANISM: Artificial Sequence
                                        KQTSS 365
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APPLICANT: Fanslow, William C.
APPLICANT: Forslow, William C.
APPLICANT: Forslow, William C.
APPLICANT: Journal C.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE '
FILE REFERENCE: 3101-A
CURRENT APPLICANTON NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENT NOS: 39
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GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300
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Pred. No. 6.4e-139;
0; Mismatches 2; Indels 0
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.5%;
Matches 363; Conservative
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LENGTH: 387
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; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fro OTHER INFORMATION: m human Nectin-3 alpha US-09-972-268-4
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APPLICANT: Baum, Peter R.

APPLICANT: Baum, Feter R.

APPLICANT: John M. William C.

APPLICANT: John M. Timothy E.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: Sorensen, Eric A.

APPLICANT: NOUNBER: US/09/972,268

CURRENT APPLICATION NUMBER: US/09/972,268

CURRENT APPLICATION NUMBER: 60/238,557

PRIOR APPLICATION NUMBER: 60/238,557

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

ENGTH: 549

TYPE: PRT
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                                                                                                                                                                                                                         DB 14; Length 549;
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Best Local Similarity 79.3%; Pred. No. 5.4e-138;
Matches 372; Conservative 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09972268; Publication No. US20030044893A1; GENERAL INFORMATION:
                      NUMBER OF SEQ ID NOS: 63
SOFWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 549
TYPE: PRT
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PRIOR FILING DATE: 2002-02-15
                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-161-572-45
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Publication No. US20030087266A1

GENERAL INFORMATION:

TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/161,572

CURRENT FILING DATE: 2002-06-03

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 60/326,605

PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR APPLICATION NUMBER: US 60/338,733

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15

PRIOR PLILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/357,253
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                    APPLICANT: Soremen, Enc. A.
APPLICANT: Soremen, Enc. A.
APPLICANT: Youakin, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF PILE REPERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT PILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 549;
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     Lofton, Timothy E.
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Best Local Similarity 79.3
Matches 372; Conservative
                                                                                                                                                                                                                                                                                              LENGTH: 549
TYPE: PRT
CRGANISM: homo sapiens
US-09-972-268-6
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US-10-161-572-45
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publication No. US20030044893A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Farmalow, William C.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Sorensen, S.
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  IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR 120
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                                                                                      VLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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Best Local Similarity 98.3%; Pred. No. 3e-136;
Matches 357; Conservative 0; Mismatches 6;
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ORGANISM: Artificial Sequence
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US-09-972-268-15
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APPLICANT: Baum, Peter R.
APPLICANT: Lofton, Timothy E.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLECTIDES, METHODS OF MAKING AND USE TITLE REFERENCE: 3101-40-05
CURRENT APPLICATION NUMBER: 00/238,557
PRIOR APPLICATION NUMBER: 00/238,557
PRIOR APPLICATION NUMBER: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 634
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     DB 10; Length 549;
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                                                    34; Indels
82.1%; Score 1888.5; DB 1(78.9%; Pred. No. 6.5e-137; ive 16; Mismatches 34;
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Publication No. US20030044893A1
GENERAL INFORMATION:
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                                                    370; Conservative
                           Similarity
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Query Match
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92.9%; Pred. No. 0; live 19; Mismatches

510; Conservative

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61 IVEPHVTAVWGKAVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSVQGDYQGR 120

VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLIKGPDS

121

61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR

1 MARTPGPAPLCPGGGKAQLSSAFPPAAGLLLPAPTPPPLLLLIPLLFSRLCGALAGSI 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFPLLLFSRLCGALAGPI

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LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR

181

GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF 300

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Best Local Similarity
Matches 510; Conserv
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Sequence 4, Appli
Sequence 6, Appli
                                                                                           7, 2005, 14:07:37; Search time 0.001 Seconds (without alignments) 821.853 Million cell updates/sec
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                                                                                                                                                                           1 MARTLRPSPLCPGGGKAQLS.........EDDLVSHVDGSVISRREWYV 549
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                  5.1.6
Compugen Ltd
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US-09-959-845-4
US-09-959-845-6
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APPLICANT: Kenicoli TRACAHASHI
TITLE CANICANT: Kenicoli TRACAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT FILING DATE: 2001-12-31
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER: OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTHE: 549
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                  GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
                                                                                                                                                                                                                                            3 segs, 1497 residues
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length: 2000000000
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Match Length DB
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510.
438
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62.5
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1814.5
1809.5
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                                                                 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
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241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPF
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APPLICANT: KEİKO SATO
APPLICANT: KEİKO SATO
APPLICANT: KEİKO SATO
APPLICANT: KEİKO SATO
APPLICANT: KEİKO SATO
SILER REFERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION UNMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR PILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENT VET. 2010-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENT VET. 2.1
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GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
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Best Local Similarity 66.4*
Matches 374; Conservative
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US-09-959-845-4
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US-09-959-845-4
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93.8%; Score 2721; DB 1; Length 549;

Query Match

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                                                                                                    VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSVQGEYQGR
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GENERAL INFORMATION:
APPLICANT: VOSNimi TAKAI
APPLICANT: HIYOVAKI NAKANISHI
APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
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APPLICANT: Keiko SATO
APPLICANT: Keiko SATO
APPLICANTON: PROCEIN NCCTIN-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT PILING DATE: 2001-103-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-065595
NUMBER: PRIOR FILING DATE: 2000-065595
NUMBER: PRIOR FILING DATE: 2000-03-09
NUMBER: PRIOR FILING DATE: 2000-03-09
SOPTWARE: PRIOR IN Ver. 2.1
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US-09-959-845-6
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US-09-959-845-6
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Perfect score:

Sequence:

Scoring table:

Searched:

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                               33; Indels
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   Pred. No. 0;
2; Mismatches
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APPLICANT: Keiko SATO
APPLICANT: Kenichi TAKAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT FILING DATE: 2001-12-31
PRIOR PFLING DATE: 2001-12-31
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 2000-065595
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
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APPLICANT: YOSHIM: TAKAL
APPLICANT: Hiroyuki NAKANISHI
al Similarity 88.8%; Pr
454; Conservative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 93.23
Matches 399; Conservative
Best Local Similarity
Matches 454; Conserv
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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GENERAL INFORMATION:
APPLICANT: YOSAİMİ TAKAI
APPLICANT: HİROYUKİ NAKANISHI
APPLICANT: Keiko SATO
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-16/80A/LC/00653
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/JPO1/01871
PRIOR APPLICATION NUMBER: PCT/JPO1/01871
PRIOR PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PALENT NOS: 14
SOFTWARE: PALENT NOS: 14
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Maximum Match 100%
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Score

Result

Database :

US-09-959-845-4

ORGANISM: Mouse

US-09-959-845-4

Query Match

Oct

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                                                                                             LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFAR
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61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHQYGFSVQGDYQGR
                                         VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORPAILOR:
APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Kesiko SATO
APPLICANT: Kesiko SATO
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US/09/09/959,845
PRIOR APPLICATION NUMBER: US/09/09/959,845
PRIOR APPLICATION NUMBER: US/09/09/97
PRIOR APPLICATION NUMBER: US/09/09/97
PRIOR APPLICATION NUMBER: US/09/09/97
PRIOR APPLICATION NUMBER: US/09/09/97
PRIOR PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
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S-09-559-845-2
Sequence 2, Application US/09959845
GENERAL INFORMATION:
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Best Local Similarity 68.2%
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